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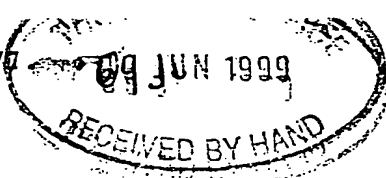
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*P. Mahoney*

Dated 2 July 2002



Wendell L.



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# Request for grant of a patent

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JEC/FP5781927  
09 JUN 1999

2. Patent application number

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**9913425.6**

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Patents ADP number (*if you know it*)

5663620001

If the applicant is a corporate body, give the country/state of its incorporation

BELGIUM

df

4. Title of the invention

IDENTIFICATION AND MOLECULAR CHARACTERISATION OF PROTEINS EXPRESSED IN THE TICK SALIVARY GLANDS

5. Name of your agent (*if you have one*)

MEWBURN ELLIS

"Address for service" in the United Kingdom to which all correspondence should be sent (*including the postcode*)

YORK HOUSE  
23 KINGSWAY  
LONDON  
WC2B 6HP

Patents ADP number (*if you know it*)

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6. If you are declaring priority from one or more earlier patent applications, give the country and the date of filing of the or of each of these earlier applications and (if you know it) the or each application number

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Number of earlier application

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8. Is a statement of inventorship and of right to grant of a patent required in support of this request? (*Answer 'Yes' if:*

YES

- a) any applicant named in part 3 is not an inventor, or
  - b) there is an inventor who is not named as an applicant, or
  - c) any named applicant is a corporate body.
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# Patents Form 1/77

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Description 53

Claim(s) 5

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Statement of inventorship and right to grant of a patent (Patents Form 7/77) 0

Request for preliminary examination and search (Patents Form 9/77) 0

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11. I/We request the grant of a patent on the basis of this application.

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Joanna Cripps

Date

8 June 1999

12. Name and daytime telephone number of person to contact in the United Kingdom JOANNA CRIPPS 0117 926 6411

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## DESCRIPTION

### Identification and molecular characterisation of proteins expressed in the tick salivary glands.

#### FIELD OF INVENTION.

The invention relates to the molecular characterisation of DNA sequences which encode proteins expressed in the salivary glands of ticks, more particularly the *Ixodes ricinus* arthropod tick. These proteins are involved in the complex mechanism of interaction between this arthropod and its mammalian host. The invention relates to newly identified polynucleotides, polypeptides encoded by them and the use of such polynucleotides and polypeptides, and to their production.

#### BACKGROUND OF THE INVENTION.

Ticks are ectoparasites which infest a large number of animals such as mammals, birds, reptiles and amphibians. They are present in almost every area of the world. The tick feeding process itself is often harmful to the host. In addition, many of these ticks are vectors of viruses, bacteria and protozoa that cause host morbidity and, in some cases, mortality, particularly in humans and livestock animals. There are three families of ticks : the *Ixodidae* or hard ticks, the *Argasidae* or soft ticks, and the *Nuttalliellidae*. The life cycle of all ticks involves four stages (egg - larva - nymph - adult). In the majority of species, as *Ixodes ricinus*, the ticks drop off the host animal after each blood meal. The larvae hatch from the eggs and

climb the vegetation where they come into easy reach of passing animals. Once on the host, they attach themselves and feed on blood. Nymphs and adults feed on other hosts and employ the same methods of host seeking. Mating of adults often takes place on the host while  
 5 attached and feeding. Egg laying occurs after detachment.

The tick salivary gland play an important role in the accomplishment of the blood meal and in the transmission of pathogens. During the blood meal, *Ixodidae* ticks concentrate the blood by using special mechanisms which eliminate the excess of  
 10 water and ions through salivary glands. A striking modification of the morphology and the physiology of the salivary glands occurs during this blood meal. The cytoplasm and the nucleus of several salivary gland cells enhance in volume leading to an important increase in the size and the weight of the salivary glands. The messenger RNA  
 15 (mRNA) synthesis is also induced, resulting in the expression of new proteins. At the end of the meal, the degeneration of the salivary glands is probably caused by the 20-hydroxyecdysone, also called "salivary degenerating factor".

The salivary gland is rich in bio-active factors : cement,  
 20 enzymes, enzyme inhibitors, histamine agonist and antagonist, anticoagulant factors, modulating factors of the host immune response, prostaglandin. Some of these interactive factors are already present in the salivary glands of unfed ticks; but others, mainly proteins, are induced during the feeding phase of the blood meal. These induced-  
 25 proteinic factors seem to play an important role in the modulation of the host immune response. One of these factors, a 65 kDa protein, was isolated by Brossard and co-workers (Ganapamo *et al.*, 1997). This protein induces, *in vitro*, a specific CD4<sup>+</sup> T cell proliferation of lymph node cells from mice infested with *I. ricinus* ticks (Ganapamo  
 30 *et al.*, 1997). These cells produce high levels of interleukin-4 (IL-4) and low levels of interferon- $\gamma$  (IFN- $\gamma$ ) when they are stimulated with concanavalin-A (Con A). This suggest a T<sub>H</sub>2 polarisation of the cytokine pattern (Ganapamo *et al.*, 1995). The production of IL-5 and IL-10 confirms this phenomenon (Ganapamo *et al.*, 1996). This  
 35 polarised response could constitute favourable conditions for the transmission of some pathogens.

The inhibition of the alternative pathway of complement activation, the decrease of the synthesis of antibodies induced by thymo-dependent antigens in infested animals, and the decrease of the proliferative activity of T-lymphocytes stimulated with mitogens, contribute to the setting up of these processes (Wikel *et al.*, 1996; Brossard and Wikel, 1997). Furthermore, prostaglandins (PGE<sub>2</sub>) and salivary proteins are involved in the suppression of the immune response. In addition, it is known that some proteinic factors expressed by the salivary glands stimulate the growth of *Borrelia burgdorferi*, the causal agent of Lyme disease, which is the main human pathogen transmitted by the *Ixodidae* ticks (De Silva *et al.*, 1995)

#### SUMMARY OF THE INVENTION.

The *Ixodes ricinus* tick is the known vector of *Borrelia burgdorferi* sensu lato, the causal agent of Lyme disease. Tick salivary glands play an important role in the blood meal and in pathogen transmission. In the salivary glands, several genes are induced during the feeding process leading to the expression of new proteins which can play an important role in the modulation of the host immune and haemostatic responses.

It is accordingly important to identify and characterize those genes which are induced during the feeding process as well as those proteins which are expressed under those circumstances and to take benefit of the interesting properties of the substances thus identified.

Accordingly, in a first aspect, the present invention relates to a method for characterising genes which are induced in the salivary glands of a tick, preferably an *Ixodes ricinus* tick, during the tick feeding phase which comprises :

a) selectively cloning mRNAs induced during the tick feeding phase to obtain a corresponding cDNA library ;

b) cloning full-length cDNAs corresponding to some incomplete cDNA sequences identified in the library obtained in step a).

5 More particularly, the genes induced are those induced during the slow-feeding phase of the blood meal.

In a preferred aspect, the method comprises :

10 a) synthesising uninduced cDNAs starting from mRNAs expressed in the salivary gland of unfed ticks ;

b) synthesising induced cDNAs starting from mRNAs expressed in the salivary gland of fed ticks ;

15 c) subtracting said uninduced cDNAs from said induced cDNAs ;

20 d) isolating and cloning specifically induced cDNAs, thus obtaining a subtractive library ;

e) obtaining corresponding full-length induced cDNA ;

25 f) sequencing and comparing said full-length induced DNA molecules with known-polypeptide and polynucleotide sequences.

30 In a further preferred aspect, a full-length cDNA library is set up and screened by means of incomplete cDNAs isolated from the subtractive library.

More particularly, the method comprises :

35 a) randomly sequencing a number of clones of said subtractive library ;



b) comparing their DNA and amino acid translated sequences with DNA and protein databases ;

c) identifying distinct family sequences ;

d) characterising their corresponding full-length mRNA sequence.

Other features of said method are described hereafter.

The sequences identified by the above described method can be divided into three classes : i) the first one refers to putative anticoagulant and anticomplementary sequences; ii) the second one refers to putative immunomodulatory sequences; iii) the last class comprises sequences presenting low or no homologies to known polynucleotide and polypeptide sequences

According to other aspects, the present invention relates to polynucleotides isolated from the tick salivary glands, polypeptides encoded by said polynucleotides as well as to the use of said polynucleotides and said polypeptides.

Said polynucleotides, said polypeptides and said uses are defined and described hereafter.

#### BRIEF DESCRIPTION OF THE DRAWINGS.

Figure 1.

RACE assay (Frohman et al., 1995) specific to Seq 16 and 24. The reverse transcription step was carried out using 10 ng of mRNAs extracted from salivary gland of engorged ticks. The brightest bands represent the cDNA fragments corresponding to the 3' end of the targeted mRNA. The amplified products were subjected to agarose gel electrophoresis followed by staining the DNA fragments by ethidium bromide. Molecular weight markers (M) were the Smart

ladder (Life technologies, Rockville, Maryland, USA). Arrows indicate the position of the expected amplified products.

5

Figure 2.

Differential expression analysis of the 5 full-length selected cDNAs and 9 cDNA fragment isolated in the subtractive library. PCR assays were carried out using as DNA template cDNAs obtained from a reverse transcription procedure on mRNAs extracted from salivary glands either of engorged (E) or of unfed (UF) ticks. These RNA messengers were also used as template in reverse transcription assays. Ten microliter of both PCR and RT-PCR mixture were subjected to agarose gel electrophoresis and ethidium bromide staining for the detection of amplified DNA products. [++] strongly positive; [+] positive; [-] negative.

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#### DESCRIPTION OF THE INVENTION.

We have characterised genes which are induced in the salivary glands of *Ixodes ricinus* during the slow-feeding phase of the blood meal. The cloning of these genes was carried out by setting up two complementary DNA (cDNA) libraries. The first one is a subtractive library based on the methodology described by Lisitsyn *et al.* (*Science* 259, 946-951, 1993) and improved by Diatchenko *et al.* (*Proc. Natl. Acad. Sci. USA* 93, 6025-6030, 1996). This library cloned selectively induced mRNA during the tick feeding phase. The second library is a full-length cDNA library which has been constructed by using the basic property of mRNAs (presence of a polyA tail in its 3' end and the cap structure in its 5' end). This cDNA library permitted the cloning of full-length cDNAs, corresponding to some incomplete

35

cDNA sequences deemed of interest, and identified in the subtractive cDNA library.

The subtractive library was set up by subtracting uninduced-cDNAs (synthesised from mRNAs expressed in the salivary glands of unfed ticks) from induced-cDNAs (synthesised from mRNAs expressed in the salivary gland at the end of the slow-feeding phase). The induced-cDNAs was digested by a restriction enzyme, divided into two aliquots, and distinctively modified by the addition of specific adapters. As for the induced-cDNAs, the uninduced cDNAs was also digested by the same restriction enzyme and then mixed in excess to each aliquot of modified induced-cDNA. Each mixture of uninduced-/induced-cDNAs was subjected to a denaturation step, immediately followed by an hybridisation step, leading to a capture of homologous induced-cDNAs by the uninduced-cDNA. Each mixture was then mixed together and subjected again to a new denaturation/hybridisation cycle. Among the hybridised cDNA molecules, this final mixture comprises induced-cDNAs with different adapters at their 5' and 3' end. These relevant cDNAs were amplified by polymerase chain reaction (PCR), using primers specific to each adapter located at each end of the cDNA molecules. The PCR products were then ligated into the pCRII™ vector by A-T cloning and cloned in an TOP-10 *E. coli* strain. The heterogeneity of this subtractive library was evaluated by sequencing the recombinant clones. The "induced" property of these cDNA sequences was checked by reverse transcription-PCR (RT-PCR) on mRNA extracted from salivary glands of engorged and unfed ticks. Finally, the full-length induced-cDNA was obtained by screening the expression library using, as a probe, some incomplete induced-cDNAs isolated from the subtractive library. These full-length induced DNA molecules were sequenced and compared to known polypeptide and polynucleotide sequences.

The full-length cDNA library was set up by using the strategy developed in the "CapFinder PCR cDNA Library Construction Kit" (Clontech). This library construction kit utilises the unique CapSwitch™ oligonucleotide (patent pending) in the first-strand synthesis, followed by a long-distance PCR amplification to generate

high yields of full-length, double-stranded cDNAs. All commonly used cDNA synthesis methods rely on the ability of reverse transcriptase to transcribe mRNA into single stranded DNA in the first-strand reaction. However, because the reverse transcriptase cannot always transcribe the entire mRNA sequence, the 5' ends of genes tend to be under-represented in cDNA population. This is particularly true for long mRNAs, especially if the first-strand synthesis is primed with oligo(dT) primers only, or if the mRNA has a persistent secondary structure. Furthermore, the use of T4 DNA polymerase to generate blunt cDNA ends after second-strand synthesis commonly results in heterogeneous 5' ends that are 5-30 nucleotides shorter than the original mRNA (D'Alessio, 1988). In the CapFinder cDNA synthesis method, a modified oligo(dT) primer is used to prime the first-strand reaction, and the CapSwitch oligonucleotide acts as a short, extended template at the 5' end for the reverse transcriptase. When the reverse transcriptase reaches the 5' end of the mRNA, the enzyme switches templates and continues replicating to the end of the CapSwitch oligonucleotide. This switching in most cases occurs at the 7-methylguanosine cap structure, which is present at the 5' end of all eukaryotic mRNAs (Furuichi & Miura, 1975). The resulting full-length single stranded cDNA contains the complete 5' end of the mRNA as well as the sequence complementary to the CapSwitch oligonucleotide, which then serves as a universal PCR priming site (CapSwitch anchor) in the subsequent amplification. The CapSwitch-anchored single stranded cDNA is used directly (without an intervening purification step) for PCR. Only those oligo(dT)-primed single stranded cDNAs having a CapSwitch anchor sequence at the 5' end can serve as templates and be exponentially amplified using the 3' and 5' PCR primers. In most cases, incomplete cDNAs and cDNA transcribed from polyA<sup>-</sup> RNA will not be recognised by the CapSwitch anchor and therefore will not be amplified.

At the end of these reactions, the full-length cDNA PCR products was ligated into the pCRII cloning vector (Invitrogen) and used for the transformation of XL2 *E. coli* strain. The full-length cDNA library was then screened by using, as a probe, the incomplete induced-cDNAs isolated from the subtractive library.

Eighty-nine clones of subtractive library were randomly sequenced, and their DNA and amino acid translated sequences were compared to DNA and protein databases. Among these, 27 distinct family sequences were identified, and 3 of them were selected for further characterisation of their corresponding full-length mRNA sequence. These 3 sequences matched the sequence of i) the human tissue factor pathway inhibitor (TFPI), ii) the human thrombin inhibitor gene, and iii) a snake venom zinc dependant metalloproteinase protein. These genes encode proteins which could be involved in the inhibition of the blood coagulation. The other 24 family sequences presented low or no homologies with polynucleotide and polypeptide sequences existing in databases. Screening of the full-length cDNA library using oligonucleotide probes specific to the 3 previously selected subtractive clones lead to the recovery of the corresponding full-length cDNAs. Random screening of this library led to the selection of 2 other clones. One is closely homologous to an interferon-like protein, whereas the other shows homologies to the *Rattus norvegicus* leucocyte common antigen related protein.

### Definitions.

“Putative anticoagulant, anti-complementary and immunomodulatory” polypeptides refer to polypeptides having the amino acid sequence encoded by the genes defined in the table. These present homologies with anticoagulant, anti-complementary and immunomodulatory polypeptides already existing in databases. These polypeptides belong to the Class I and Class II sequences (see table)

“Putative anticoagulant, anti-complementary and immunomodulatory” cDNAs refer to polynucleotides having the nucleotide sequence defined in the table, or allele variants thereof and/or their complements. These present homologies with anticoagulant, anti-complementary and immunomodulatory polynucleotides already existing in databases. These cDNAs belong to the Class I and Class II sequences (see table)

Some polypeptide or polynucleotide sequences present low or no homologies with already existing polypeptides or polynucleotides in databases. These belong to the Class III (see table).

« Polypeptide » refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. “Polypeptide” refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. “Polypeptides” include amino acid sequences modified either by natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be

appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications.

Polypeptides may be branched as a result of ubiquitination, and they  
 5 may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from posttranslational natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a hem moiety, covalent  
 10 attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-linkings, formation of cystine, formation of pyroglutamate, formylation,  
 15 gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. See,  
 20 for instance, PROTEINS – STRUCTURE AND MOLECULAR PROPERTIES, 2<sup>nd</sup> Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993 and Wolt, F., Posttranslational Protein Modifications : Perspectives and Prospects, pgs. 1-12 in POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed.,  
 25 Academic Press, New York, 1983; Seifter *et al.*, “Analysis for protein modifications and nonprotein cofactors”, *Meth Enzymol* (1990) 182 : 626-646 and Rattan *et al.*, “Protein Synthesis : Posttranslational Modifications and Aging”, *Ann NY Acad Sci* (1992) 663 : 48-62.

30 “Polynucleotide” generally refers to any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA.  
 “Polynucleotides” include, without limitation single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double- stranded RNA, and RNA that is a mixture  
 35 of single- and double-stranded regions, hybrid molecules comprising

DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, "Polynucleotide" refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The term Polynucleotide also  
5 includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications has been made to DNA and RNA; thus, "Polynucleotide" embraces chemically,  
10 enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide" also embraces relatively short polynucleotides, often referred to as oligonucleotides.

15  
"Variant" as the term is used herein, is a Polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide respectively, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from  
20 another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference  
25 sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions identical. A variant and reference polypeptide may  
30 differ in amino acid sequence by one or more substitutions (preferably conservative), additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant  
35 that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis



techniques or by direct synthesis. Variants should retain one or more of the biological activities of the reference polypeptide. For instance, they should have similar antigenic or immunogenic activities as the reference polypeptide. Antigenicity can be tested using standard immunoblot experiments, preferably using polyclonal sera against the reference polypeptide. The immunogenicity can be tested by measuring antibody responses (using polyclonal sera generated against the variant polypeptide) against purified reference polypeptide in a standard ELISA test. Preferably, a variant would retain all of the above biological activities.

"Identity" is a measure of the identity of nucleotide sequences or amino acid sequences. In general, the sequences are aligned so that the highest order match is obtained. "Identify" *per se* has an art-recognized meaning and can be calculated using published techniques. See, e.g. : (COMPUTATIONAL MOLECULAR BIOLOGY, Lesk, A.M., ed., Oxford University Press, New York, 1988; BIOCOMPUTING : INFORMATICS AND GENOME PROJECTS, Smith, D.W., ed., Academic Press, New York, 1993; COMPUTER ANALYSIS OF SEQUENCE DATA, PART I, Griffin, A.M., and Griffin, H.G., eds, Humana Press, New Jersey, 1994; SEQUENCE ANALYSIS IN MOLECULAR BIOLOGY, von Heijne, G., Academic Press, 1987; and SEQUENCE ANALYSIS PRIMER, Gribskov, M. and Devereux, J., eds, M Stockton Press, New York, 1991). While there exist a number of methods to measure identity between two polynucleotide or polypeptide sequences, the term "identity" is well known to skilled artisans (Carillo, H., and Lipton, D., *SIAM J Applied Math* (1998) 48 : 1073). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in Guide to Huge Computers, Martin J. Bishop, ed., Academic Press, San Diego, 1994, and Carillo, H., and Lipton, D., *SIAM J Applied Math* (1988) 48 : 1073. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux, J., *et al.*, *J Molec Biol*

(1990).215 : 403). Most preferably, the program used to determine identity levels was the GAP program, as was used in the Examples below.

5                   As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity" to a reference nucleotide sequence is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include an average up to five point  
10 mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of  
15 nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the  
20 reference sequence or in one or more contiguous groups within the reference sequence.

#### **Polypeptides of the invention.**

25                   The present invention relates to proteins (or polypeptides) secreted by *I. ricinus* salivary glands. These polypeptides include the polypeptides encoded by the cDNAs defined in the table; as well polypeptides comprising the amino acid sequence encoded by the  
30 cDNAs defined in the table; and polypeptides comprising the amino acid sequence which have at least 75 % identity to that encoded by the cDNAs defined in the table over their entire length, and preferably at least 80 % identity, and more preferably at least 90 % identity. Those with 95-99 % are highly preferred.

35                   The *I. ricinus* salivary gland polypeptides may be in the form of the "mature" protein or may be a part of a larger protein such

as a fusion protein. It may be advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which help in purification such as multiple histidine residues, or an additional sequence for stability during  
5 recombinant production.

Fragments of the *I. ricinus* salivary gland polypeptides are also included in the present invention. A fragment is a polypeptide having an amino acid sequence that is the same as part,  
10 but not all, of the amino acid sequence of the aforementioned *I. ricinus* salivary gland polypeptides. As with *I. ricinus* salivary gland polypeptides, fragment may be "free-standing" or comprised within a larger polypeptide of which they form a part or region, most preferably as a single continuous region. Representative examples of  
15 polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, and 101 to the end of the polypeptide. In this context "about" includes the particularly recited ranges larger or smaller by several, 5, 4, 3, 2 or 1 amino acid at either extreme or at both extremes.

20

Preferred fragments include, for example, truncation polypeptides having the amino acid sequence of the *I. ricinus* salivary gland polypeptides, except for deletion of a continuous series of residues that includes the amino terminus, or a continuous series of  
25 residues that includes the carboxyl terminus and / or transmembrane region or deletion of two continuous series of residues, one including the amino terminus and one including the carboxyl terminus. Also preferred are fragments characterised by structural or functional attributes such as fragments that comprise alpha-helix and alpha-helix  
30 forming regions, beta-sheet and beta-sheet forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Other  
35 preferred fragments are biologically active fragments. Biologically active fragments are those that mediate *I. ricinus* salivary gland

protein activity, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Also included are those that antigenic or immunogenic in an animal or in a human.

5                    Preferably, all of these polypeptide fragments retain parts of the biological activity (for instance antigenic or immunogenic) of the *I. ricinus* salivary gland polypeptides, including antigenic activity. Variants of the defined sequence and fragments also form part of the present invention. Preferred variants are those that vary from the  
10                    referents by conservative amino acid substitutions – i.e., those that substitute a residue with another of like characteristics. Typical such substitutions are among Ala, Val, Leu and Ile; among Ser and Thr; among the acidic residues Asp and Glu; among Asn and Gln; and among the basic residues Lys and Arg; or aromatic residues Phe and  
15                    Tyr. Particularly preferred are variants in which several, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination. Most preferred variants are naturally occurring allelic variants of the *I. ricinus* salivary gland polypeptide present in *I. ricinus* salivary glands.

20                    The *I. ricinus* salivary gland polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides  
25                    produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

#### **Polynucleotides of the invention.**

30                    Another aspect of the invention relates to *I. ricinus* salivary gland cDNAs (polynucleotides). These include isolated polynucleotides which encode *I. ricinus* salivary gland polypeptides and fragments respectively, and polynucleotides closely related thereto. More specifically, *I. ricinus* salivary gland cDNAs of the  
35                    invention include a polynucleotide comprising the nucleotide sequence of cDNAs defined in the table, encoding a *I. ricinus* salivary gland

polypeptide. The *I. ricinus* salivary gland cDNAs further include a polynucleotide sequence that has at least 75% identity over its entire length to a nucleotide sequence encoding the *I. ricinus* salivary gland polypeptide encoded by the cDNAs defined in the table, and a  
5 polynucleotide comprising a nucleotide sequence that is at least 75% identical to that of the cDNAs defined in the table. In this regard, polynucleotides at least 80% identical are particularly preferred, and those with at least 90% are especially preferred. Furthermore, those with at least 95% are highly preferred and those with at least 98-99%  
10 are most highly preferred, with at least 99% being the most preferred, with at least 99% being the most preferred. Also included under *I. ricinus* salivary gland cDNAs is a nucleotide sequence which has sufficient identity to a nucleotide sequence of a cDNA defined in the table to hybridize under conditions useable for amplification or for  
15 use as a probe or marker. The invention also provides polynucleotides which are complementary to such *I. ricinus* salivary gland cDNAs.

The nucleotide sequence encoding *I. ricinus* salivary gland polypeptide encoded by the cDNAs defined in the table may be  
20 identical to the polypeptide encoding sequence contained in the genes defined in the table, or it may be a sequence, which as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide encoded by the genes defined in the table respectively.

25 When the polynucleotides of the invention are used for the recombinant production of an *I. ricinus* salivary gland polypeptide, the polynucleotide may include the coding sequence for the mature polypeptide or a fragment thereof, by itself; the coding sequence for the mature polypeptide or fragment in reading frame with other coding  
30 sequences, such as those encoding a leader or secretory sequence, a pre-, or pro- or preproprotein sequence, or other fusion peptide portions. For example, a marker sequence which facilitates purification of the fused polypeptide can be encoded. In certain preferred embodiments of this aspect of the invention, the marker  
35 sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al*, *Proc Natl Acad Sci USA*

(1989) 86:821-824, or is an HA tag, or is glutathione-s-transferase. The polynucleotide may also contain non-coding 5' and 3' sequences, such as transcribed, non-translated sequences, splicing and polydenylation signals, ribosome binding sites and sequences that stabilize mRNA.

Further preferred embodiments are polynucleotides encoding *I. ricinus* salivary gland protein variants comprising the amino acid sequence of the *I. ricinus* salivary gland polypeptide encoded by the cDNAs defined by the table respectively in which several, 10-25, 5-10, 1-5, 1-3, 1-2 or 1 amino acid residues are substituted, deleted or added, in any combination. Most preferred variant polynucleotides are those naturally occurring *I. ricinus* sequences that encode allelic variants of the *I. ricinus* salivary gland proteins in *I. ricinus*.

The present invention further relates to polynucleotides that hybridize to the herein above-described sequences. In this regard, the present invention especially relates to polynucleotides which hybridize under stringent conditions to the herein above-described polynucleotides. As herein used, the term "stringent conditions" means hybridisation will occur only if there is at least 80%, and preferably at least 90%, and more preferably at least 95%, yet even more preferably 97-99% identity between the sequences.

Polynucleotides of the invention which are identical or sufficiently identical to a nucleotide sequence of any gene defined in the table or a fragment thereof, may be used as hybridisation probes for cDNA clones encoding *I. ricinus* salivary gland polypeptides respectively and to isolate cDNA clones of other genes (including cDNAs encoding homologs and orthologs from species other than *I. ricinus*) that have a high sequence similarity to the *I. ricinus* salivary gland cDNAs. Such hybridisation techniques are known to those of skill in the art. Typically these nucleotide sequences are 80% identical, preferably 90% identical, more preferably 95% identical to that of the referent. The probes generally will comprise at least 15

nucleotides. preferably, such probes will have at least 30 nucleotides and may have at least 50 nucleotides. Particularly preferred probes will range between 30 and 50 nucleotides. In one embodiment, to obtain a polynucleotide encoding *I. ricinus* salivary gland polypeptide, including homologs and orthologs from species other than *I. ricinus*, comprises the steps of screening an appropriate library under stringent hybridisation conditions with a labelled probe having a nucleotide sequence contained in one of the gene sequences defined by the table, or a fragment thereof; and isolating full-length cDNA clones containing said polynucleotide sequence. Thus in another aspect, *I. ricinus* salivary gland polynucleotides of the present invention further include a nucleotide sequence comprising a nucleotide sequence that hybridise under stringent condition to a nucleotide sequence having a nucleotide sequence contained in the cDNAs defined in the table, or a fragment thereof. Also included with *I. ricinus* salivary gland polypeptides are polypeptides comprising amino acid sequences encoded by nucleotide sequences obtained by the above hybridisation conditions. Such hybridisation techniques are well known to those of skill in the art. Stringent hybridisation conditions are as defined above or, alternatively, conditions under overnight incubation at 42°C in a solution comprising : 50% formamide, 5xSSC (150mM NaCl, 15mM trisodium citrate), 50mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 microgram/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1xSSC at about 65°C.

The polynucleotides and polypeptides of the present invention may be employed as research reagents and materials for discovery of treatments and diagnostics to animal and human disease.

### Diagnostic Assays

This invention also relates to the use of *I. ricinus* salivary gland polypeptides, or *I. ricinus* salivary gland polynucleotides, for use as diagnostic reagents.

Materials for diagnosis may be obtained from a subject's cells, such as from blood, urine, saliva, tissue biopsy.

Thus in another aspect, the present invention relates to a  
5 diagnostic kit for a disease or susceptibility to a disease which  
comprises :

(a) an *I. ricinus* salivary gland polynucleotide, preferably  
the nucleotide sequence of one of the gene sequences defined by the  
table, or a fragment thereof;

10 (b) a nucleotide sequence complementary to that of(a);

(c) an *I. ricinus* salivary gland polypeptide, preferably the  
polypeptide encoded by one of the gene sequences defined in the  
table, or a fragment thereof;

(d) an antibody to an *I. ricinus* salivary gland  
15 polypeptide, preferably to the polypeptide encoded by one of the gene  
sequences defined in the table; or

(e) a phage displaying an antibody to an *I. ricinus*  
salivary gland polypeptide, preferably to the polypeptide encoded by  
one of the cDNAs sequences defined in the table.

20

It will be appreciated that in any such kit, (a), (b), (c), (d)  
or (e) may comprise a substantial component.



The anti-*I. ricinus* salivary gland polypeptide antibodies may comprise polyclonal antibodies.

Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the *I. ricinus* salivary gland polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized.

Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL TDM adjuvant. The immunization protocol may be selected by one skilled in the art without undue experimentation.

The anti-*I. ricinus* salivary gland polypeptide antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro.

The immunizing agent will typically include the *I. ricinus* salivary gland polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Rockville, Maryland. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J

Immunol, 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against *I. ricinus* salivary gland polypeptide. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively the hybridoma cells may be grown in *vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., supra] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

As an alternative or supplement to immunising a mammal with a peptide, an antibody specific for a protein may be obtained from a recombinantly produced library of expressed immunoglobulin variable domains, e.g. using lambda bacteriophage or filamentous bacteriophage which display functional immunoglobulin binding domains on their surfaces; for instance see WO92/01047. The library may be naive, that is constructed from sequences obtained from an organism which has not been immunised with any of the proteins (or fragments), or may be one constructed using sequences obtained from an organism which has been exposed to the antigen of interest.

### Vaccines.

Another aspect of the invention relates to a method for inducing an immunological response in a mammal which comprises inoculating the mammal with *I. ricinus* salivary gland polypeptide or epitope-bearing fragments, analogs, outer-membrane vesicles or cells (attenuated or otherwise), adequate to produce antibody and/or T cell immune response to protect said animal from bacteria and viruses which could be transmitted during the blood meal of *I. ricinus* and related species. In particular the invention relates to the use of *I. ricinus* salivary gland polypeptides encoded by the cDNAs defined in the table. Yet another aspect of the invention relates to a method of inducing immunological response in a mammal which comprises,

delivering *I. ricinus* salivary gland polypeptide via a vector directing expression of *I. ricinus* salivary gland polynucleotide *in vivo* in order to induce such an immunological response to produce antibody to protect said animal from diseases (Lyme disease, tick encephalitis virus disease, ....).

A further aspect of the invention relates to an immunological composition or vaccine formulation which, when introduced into a mammalian host, induces an immunological response in that mammal to a *I. ricinus* salivary gland polypeptide wherein the composition comprises a *I. ricinus* salivary gland cDNA, or *I. ricinus* salivary gland polypeptide or epitope-bearing fragments, analogs, outer-membrane vesicles or cells (attenuated or otherwise). the vaccine formulation may further comprise a suitable carrier. The *I. ricinus* salivary gland polypeptide vaccine composition is preferably administered orally or parenterally (including subcutaneous, intramuscular, intravenous, intradermal etc. injection). Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the blood of the recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example; sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity to the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

Yet another aspect relates to an immunological/vaccine formulation which comprises the polynucleotide of the invention. Such techniques are known in the art, see for example Wolff *et al* , *Sciences*, (1990) 247 : 1465-8.

### Therapeutics.

Another aspect of the invention relates to the use of these *I. ricinus* salivary gland polypeptides as therapeutics agent. In considering the particular potential therapeutic areas for the likely products, the hospital disciplines cover by these products are : haematology (particularly coagulation clinics), transplantation (for immunosuppression control), rheumatology (for anti-inflammatories), and general treatment (for specific or improved anesthetics).

10

Gene	Motives	Similar sequences in databases	Score	Class
Seq. 1		No significant identity		III
Seq. 2		No significant identity		III
Seq. 3		No significant identity		III
Seq. 4		No significant identity		III
Seq. 5		No significant identity		III
Seq. 6		Prokariotic mbne lipoprotein lipid attachment site		III
		R. melioli Nitrogen fixation (fixF)	0.00089	III
		Human Apolipoprotein B-100	0.0045	III
		Hu. mRNA for cAMP response element (CRE-BP1) binding prot	0.057	III
Seq. 7	Kunitz family of serine protease inhibitor	Human BAC clone GS345D13	4.7 <sup>13</sup>	I
		H. sap Tissue factor Pathway Inhibitor PI-2	4 <sup>12</sup>	I
Seq. 8		No significant identity		III
Seq. 9	Prokariotic mbne lipoprotein lipid attachment site	Pea mRNA for GTP binding prot.	0.48	III
Seq. 10		No significant identity		III
Seq. 11		IL-11 R-Béla gene	0.18	II
Seq. 12		No significant identity		III
Seq. 13		C. gloeosporioides cutinase gene	0.082	III
Seq. 14		No significant identity		III
Seq. 15		Mouse mRNA for secretory prot cont. transpondine motifs	0.014	III
Seq. 16	Zinc dependent metalloproteinase family	B. jararaca mRNA for jararagin	1.1 <sup>5</sup>	I
		Agkistrodon contortrix metalloproteinase precursor	3.9 <sup>5</sup>	I
Seq. 17		O. aries gene for ovine INF-alpha	0.7	II
		Interferon-omega 45	0.88	II
		Interferon-omega20	0.89	II
		RCPT PGE2	0.85	III
		PGE Rept EP2	0.85	III
Seq. 18		No significant identity		III
Seq. 19		IgG1 L chain directed against human IL2 repl Tac prot	0.19	II
		Var region of light chain of MAK447/179	0.2	II
Seq. 20		No significant identity		III
Seq. 21		No significant identity		III
Seq. 22		Mus Musculus neuroactin	0.42	III
Seq. 23		No significant identity		III
Seq. 24		H. sapiens thrombin inhibitor	2.1 <sup>12</sup>	I
		Cytoplasmic antiproteinase 38 kDa intracellular serine prot.	2.3 <sup>12</sup>	I
Seq. 25		No significant identity		III
Seq. 26		No significant identity		III
Seq. 27		Mus musculus transcription factor ELF3 (fasta)	0.053	III
Seq. 28		Homo sapiens putative interferon-related protein (SM15) mRNA	1.70E-22	II
Seq. 29		(R) norvegetics mRNA for leucocyte common antigen-related protein	4.00E-09	II

Class I: putative anticoagulant homologs; Class II: putative immunomodulatory homologs; Class III: low or no homologs found in the databases.

## EXAMPLES

## Biological materials used in this study.

5           The salivary glands of 5 day engorged or unfed free of  
pathogen *Ixodes ricinus* female adult ticks were used in this work.  
When removed, these glands were immediately frozen in liquid  
nitrogen and stored at  $-80^{\circ}\text{C}$ . To extract RNA messengers (mRNA),  
the salivary glands were crushed in liquid nitrogen using a mortar and  
10 a pestle. The mRNAs were purified by using an oligo-dT cellulose  
(Fast Track 2.0 kit, Invitrogen, Groningen, The Netherlands). Two  
micrograms of mRNAs were extracted from 200 salivary glands of fed  
ticks; and  $1.5\text{ }\mu\text{g}$  of mRNAs were also extracted from 1,000 salivary  
glands of unfed ticks.

15

Example 1 : Construction of a Representational  
Difference Analysis (RDA) subtractive library.

20           All procedures were performed as described by Hubank  
and Schatz (1994). Double-stranded cDNAs were synthesised using  
the Superscript Choice System (Life Technologies, Rockville,  
Maryland, USA). The cDNAs were digested with DpnII restriction  
enzyme, ligated to R-linkers, amplified with R-24 primers (Hubank  
25 and Schatz, 1994), and finally digested again with the same enzyme to  
generate a "tester" pool consisting of cDNAs from salivary glands of  
fed ticks and a "driver" pool consisting of cDNAs from salivary  
glands of unfed ticks. The first round of the subtractive hybridisation  
process used a tester/driver ratio of 1:100. The second and third  
30 rounds utilised a ratio of 1:400 and 1:200,000, respectively. After  
three cycles of subtraction and amplification, the DpnII-digested  
differential products were subdivided according to size into 4 different  
fractions on a 1.7% electrophoresis agarose gel, and subcloned into  
the BamHI site of the pTZ19r cloning vector. The ligated product was  
35 used to transform TOP-10 *E. coli* competent cells (Invitrogen,  
Groningen, The Netherlands). Nine thousand six hundred clones of

this subtractive library were randomly selected, and individually put in 100 microplates and stored at -80°C. This subtractive library was analysed by sequencing 89 randomly chosen clones, using M13 forward and reverse primers specific to a region located in the pT19r cloning vector. The DNA sequences of these 89 clones were compared, and 27 distinct family sequences were identified. Homology of these sequences to sequences existing in databases is presented in Table 1. The subtractive sequences 1 to 27 are presented in the sequence-listing file (except for sequences 16 and 24 whose complete mRNA sequences are presented; see section, Example 2). Three sequences (Seq 7, 16 and 24) were selected for further characterisation of their corresponding full-length mRNA sequence. These 3 sequences matched the sequence of i) the human tissue factor pathway inhibitor (TFPI), ii) a snake venom zinc dependant metallopeptidase protein, and iii) the human thrombin inhibitor protein, corresponding to Seq 7, 16 and 24, respectively. These genes encode proteins which could be involved in the inhibition of the blood coagulation. The other 23 family sequences presented low or no homologies with polynucleotide and polypeptide sequences existing in databases

20

Example 2 : Construction of the full length cDNA library and recovery of full length cDNAs sequences by screening of this full length cDNA library.

25

This library was set up using mRNAs extracted from salivary glands of engorged ticks. The mRNAs (80 ng) were subjected to reverse transcription using a degenerated oligo-dT primer (5'-A(T)30VN-3'), the SmartTM oligonucleotide (Clontech, Palo Alto, USA), and the Superscript II reverse transcriptase (Life Technologies, Rockville, Maryland, USA). The single strand cDNA mixture was used as template in a hot start PCR assay including the LA Taq polymerase (Takara, Shiga, Japan), the modified oligo-dT primer and a 3'-'Smart' primer specific to a region located at the 5' end of the SmartTM oligonucleotide. The PCR protocol applied was : 1 min at 95°C, followed by 25 sec at 95°C / 5 min at 68°C, 25 times, and 10 min at

35



72°C. The amplified double stranded cDNA mixture was purified with a Centricon 30 concentrator (Millipore, Bedford, USA). The cDNAs were divided into 4 fractions ranging from 0.3 to 0.6 kb, 0.6 to 1 kb, 1 kb to 2 kb and 2 kb to 4 kb on a 0,8% high grade agarose  
 5 electrophoresis gel and recovered separately by using the Qiaex II extraction kit (Qiagen, Hilden, Germany). The 4 fractions were ligated individually into the pCRII cloning vector included in the TOPO cloning kit (Invitrogen, Groningen, The Netherlands). The ligated fractions were then used to transform XL2-Blue ultracompetent *E. coli*  
 10 cells (Stratagene, Heidelberg, Germany). The resulted recombinant clones were stored individually in microplates at -80°C. Ten clones were randomly chosen for partial or complete sequencing. As a result of this procedure, 2 cDNA sequences (Seq 28 and Seq 29, see Table 1) were selected for their homology to sequence databases. One is  
 15 closely homologous to an interferon-like protein (Seq 28), whereas the other shows homologies to the *Rattus norvegicus* leucocyte common antigen-related protein (Seq 29).

The 4 different fractions of the full-length cDNA library  
 20 were screened with radio-labelled oligonucleotide probes. The labelling of these oligo probes was performed as described in Current Protocols in Molecular Biology (Ausubel et al, 1995, J. Wiley and  
 sons, Eds). These 4 different fractions were then plated on nitrocellulose membranes and grown overnight at 37°C. These  
 25 membranes were denatured in NaOH 0.2M / NaCl 1.5M, neutralised in Tris 0.5M pH 7.5-NaCl 1.5M and fixed in 2X SSC (NaCl 0.3 M/ Citric Acid Trisodium di-hydrated 0.03 M). The membranes were heated for 90 min. at 80°C, incubated in a pre-hybridisation solution (SSC 6X, Denhardt's 10X, SDS 0,1%) at 55°C for 90 min., and finally put  
 30 overnight in a preheated hybridisation solution containing a specific radio-labelled oligonucleotide probe at 55 °C. The hybridised membranes were washed 3 times in a SSC 6X solution at 55 °C for 10 min, dried and exposed on Kodak X-OMAT film overnight at -80°C. In this way, the complete consensus mRNA sequence of the Seq 28  
 35 and 29 was confirmed by the recovery of two other clones corresponding to these sequences. Only one full-length cDNA clone

corresponding to the subtractive clone 16 was isolated. Therefore, to identify the complete sequence of the Seq 16 and 24, the Rapid Amplification of cDNA Ends (RACE) method was applied.

5                   The RACE methodology was performed as described by Frohman et al. (1995). The reverse transcription step was carried out using 10 ng of mRNAs extracted from salivary gland of engorged ticks and the Thermoscript Reverse transcriptase (Life technologies, Rockville, Maryland, USA). All gene specific primers (GSP) had an  
10   18 base length with a 61% G/C ratio. The amplified products were subjected to an agarose gel electrophoresis and recovered by using an isotachophorese procedure. The cDNAs were cloned into the pCRII-TOPO cloning vector (Invitrogen, Groningen, The Netherlands). To  
15   identify the consensus cDNA sequence, different clones were sequenced., and their sequence was compared to their known corresponding sequence. Therefore, the complete cDNA sequences of the clones 16 and 24 isolated in the subtractive library were obtained by this RACE procedure (figure 1).

20

Example 4 : Evaluation of the differential expression of the cDNA clones isoalted in the subtractive and full-length cDNA libraries.

25                   The differential expression of the mRNAs corresponding to the 5 full-length selected clones (Seq 7, 16, 24, 28 and 29) and of 9 subtractive clones was assessed using a PCR and a RT-PCR assays (figure 2).

30                   The PCR assays were carried out using as DNA template cDNAs obtained from a reverse transcription procedure on mRNAs extracted from salivary glands either of engorged or of unfed ticks. Each PCR assay included pair of primers specific to each target subtractive or cDNAs full-length sequence. PCR assays were  
35   performed in a final volume of 50 µl containing 1µM primers, 0.2 mM deoxynucleotide (dATP, dCTP, dGTP and dTTP; Boehringer

Mannheim GmbH, Mannheim, Germany), PCR buffer (10 mM Tris-HCl, 50 mM KCl, 2.5 mM MgCl<sub>2</sub>, pH 8.3) and 2.5 U of Taq DNA polymerase (Boehringer Mannheim GmbH, Mannheim, Germany). DNA samples were amplified for 35 cycles under the following  
 5 conditions : 94°C for 1 min., 72 °C for 1 min. and 64 °C for 1 min, followed by a final elongation step of 72 °C for 7 min.

The RT-PCR assay was carried out on the 5 selected full-length cDNA clones and on 5 cDNA subtractive clones. The mRNAs  
 10 used as template in the reverse transcription assay was extracted from salivary glands of engorged and unfed *I. ricinus* ticks. The reverse transcription assays were performed using a specific primer (that target one the selected sequences) and the "Thermoscript Reverse transcriptase" (Life technologies, Rockville, Maryland, USA) at 60°C  
 15 for 50 min. Each PCR assay utilised the reverse transcription specific primer and an another specific primer. The PCR assays were performed in a final volume of 50 µl containing 1µM primers, 0.2 mM deoxynucleotide (dATP, dCTP, dGTP and dTTP; Boehringer Mannheim GmbH, Mannheim, Germany), PCR buffer (10 mM Tris-  
 20 HCl, 50 mM KCl, 2.5 mM MgCl<sub>2</sub>, pH 8.3) and 2.5 U of Expand High Fidelity polymerase (Roche, Bruxelles, Belgium). Single stranded DNA samples were amplified for 30 cycles under the following conditions : 95°C for 1 min., 72 °C for 30 sec. and 60 °C for 1 min, followed by a final elongation step of 72 °C for 7 min. The  
 25 figure 2 shows that the expression of the selected sequences is induced in salivary glands of 5 day engorged ticks, except for the sequence 28 that is expressed at a similar level in salivary glands of engorged and unfed ticks.

## SEQUENCE LISTING

## (1) INFORMATION FOR SEQ ID N°: 1

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 194 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°1 :

```

1  ATACCTTCCA CTTGTAGCCC TTCCTCATCC GATATGGTGA CGGATGCCAT
51 TGCATCCTCG TCGTGGAAGA GGTCCTCTTC TAAATAAGAC CCATCCATAT
101 ATGTGTGTTT GCGAATGCCG TCGACGTAGC TCCTGACTAG AAACTCGTGC
151 GCTAGGACAG AACTTTTCTT CAGGTTTAGC GTAATGTCCT CGTT

```

## (2) INFORMATION FOR SEQ ID N°: 2

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 607 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°2 :

```

1  TACCNGGGAA TCCAAAACCA ATTTTATTG GAACTTCCAC GTCTTCTTCA
51 AGGCGGTGGC ACCTCTGCAT TTATGAAGTT CGTCTTGGCA TTTTATTTTT
101 TGCTTCTTTC ATTGCRGAAC TCGCAAATGC ACTTCCCGTG CTTGTCGCAT
151 TTCGCCCCAA AAGCGCATGG CATTCCTTCC GGCAGATTAA CTTTTTCAAA
201 TTCACGGTTC TGAACCAATA ATAGATCGTG GCAATGTTTG TGCTGTTTGC
251 GATTTGCAAA CCAGCTGTAG CCACCATTGG ACTCAAAGGT GCGCACAACA
301 TGGCGCCGAA CTGTGAAAAA CAAATTAAGG CTNCTTTGTA ATAACGCTAG
351 TCTTGGTACG CCGTTAGAGG TCGATGTCGC GCCTCGCGAT TGCAAAGTCA
401 CTTGCACTTA TCAAGCTCCT GGAGAAAAAT GGGTGCAACG GGGGGATCAG
451 CGTTTGTACT TGCAAACATT TGTGGAGACG GTAAACCWGT ATTTTCGCGGA
501 ACTCAGATGC TCCAGCGTGA AGCTCGTCTT AATAAAAGTT GTAAATTCGA

```

551 GTATNGATGA AGAACTGAAA TTCGAGGCAT TTAGAAACAC CACGAGAAGC  
601 AGCGGAA

5

## (3) INFORMATION FOR SEQ ID N°: 3

## (i) SEQUENCE CHARACTERISTICS :

- 10 (a) LENGTH : 259 base pairs  
(b) TYPE : nucleic acid  
(c) STRANDEDNESS : single  
(d) TOPOLOGY : linear

## 15 (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°3 :

20 1 GATCCTACGC CTGAAAATGA GTGTCCATCG TCTTCACATA GTGCCACATT  
51 GTAATTGGTA CAAGCTCCAT TTTCGTCAGC GCTGTTTGTT ATGCTGCCGC  
101 CTACTTTTCC TTCGGCACTC CATAAGTTAA ACCCTGTCAT TATAAGTGTG  
25 151 ATTGCCGTAT CTCGGCTGAA TGGGTTCCAT TTTTCTCTTA AATAATCACG  
201 TGTCCATATT CCATGTATTG TGTTCATGAG TATGTGATTC TCATCGTATA  
30 251 TCTTCGCCT

## (4) INFORMATION FOR SEQ ID N°: 4

## 35 (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 170 base pairs  
(b) TYPE : nucleic acid  
(c) STRANDEDNESS : single  
40 (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°4 :

45 1 CCACTCGAAA ATGGAGGCTT TGAAACATTT CAGTACCCCT GTGAACTCTG  
51 GCTTTGCAAT GTAACAGCAA AAACACTTAC AGTTGAAGGG TGCAGTGTCA  
101 GACGCTATGG AAGTTGCATC CACGAGCACR ACCCTGATTA CTACTGGCCA  
50 151 CGTTGCTRTC CGGGTCGTCC

## (5) INFORMATION FOR SEQ ID N°: 5

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 168 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°5 :

1 GTATGTTACC ATGTCCAACC CGGTTATTAA ATACACCAAG TCGTAGGATT  
 51 TGTAGGCAGC TGCATTGCCC TTGACGTACT CTCTCAACGT TGCCAAGGAC  
 101 TCAGGCCCAT AAATGTAGTG GGGTTGACCT TGAACCTCTC GTAAAAAGCG  
 151 TTCTTTCTCC GTCGTGAG

## (6) INFORMATION FOR SEQ ID N°: 6

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 247 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°6 :

1 CCGAAMATAA AACTTAGTCT CACCAATATA CGTTTGCCTA ACGCGAAGGA  
 51 ACAGGCACAA ATATACTACG AGCACGACAT TCTCAAGAAC ACGGTTACAG  
 101 GAGTGTGGAC GAGAATTCAC TCAAAATATC CGTTCCTGA AGATGAGGGA  
 151 ATTACACTGA TAATGACAGG GTTTGATTTA TGGAGTGCCG ATTAACTGT  
 201 AGGCGGCACC ATAACAAACA GCGCTGAGAA AAGCGGAGCT TGTACGA

## (7) INFORMATION FOR SEQ ID N°: 7

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 351 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°7 :

```

1   CTTCTGGTGT AGCTTAGTCA TTGTGGCCTG CATCGTGGTA GACACAGCCA
15  51  ACCACAAAGG TAGAGGGCGG CCTGCGAAGT GTAAACTTCC TCCGGACGAC
    101  GGACCATGCA GAGCACGAAT TCCGAGTTAC TACTTTGATA GAAAAACCAA
    151  AACGTGCAAG GAGTTTATGT ATGGCGGATG CGAAGGAAAC GAAAAACAATT
20  201  TTGAAAACAT AACTACGTGC CAAGAGGAAT GCAGAGCAAA AAAAGTCTAA
    251  ACCAAGCCTT GAATGAAGAC TGCCTGAGAT CATTCAAGAA GAATCTGTGC
25  301  TCAGTCAAAT AAGACAAAAA GTCAAATAAT AAAATAAGTT TAAAAAATC
    351  G

```

## (8) INFORMATION FOR SEQ ID N°: 8

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 292 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°8 :

```

1   CATCGMAGCC ATAGTATATT TTGCACTTGT CTTCCGTTTC GTCGTAGTAG
45  51  GACCGATTCC ACATTGTAGT ACACCAGTCA CTTATATCCT GCGGGCGGTT
    101  CTTGCATTTG TCCTGAACAA ATCTTCCACA GCGCTTGTCG CACGCCTCCT
    151  GGGAAATAGAA CGCGTTCTCT CCTCCGCATC TCCATTTGGA ATCATAGAAA
50  201  CATCTTTTCA TTTGAATATT GTAGCGATAA TAATCGGTAT CAGTTTCTTT
    251  GCATGGTCCT GGGAGGGGTT TGGCGCAGGG GCCGTATTCA GG

```

## (9) INFORMATION FOR SEQ ID N°: 9

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 270 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°9 :

```

1  GGTAATAGTT GTCAAATTCC ATTAATGTAT CCTGAAATGT GACCATATCT
15  51  TTGTTTCCCC TGTAATCTCT CATAAAAGGC TGTGTGTTTT CCTTAAGAAG
    101  TGTAACAGCC ACGATGGTCA ATCTCACGGA TGGATGTGTG ACACTTTTAT
    151  ATCTCAGGTT TGCCGACATT GCCATTACAG ATAAATAGTT GATAATTTCT
20  201  TTCTTGTTAT AGTTGTAAGC AGCGCATGTT GTTGCATCAA GCACCACATG
    251  CACTTCAGGC AATATGGTTT

```

## (10) INFORMATION FOR SEQ ID N°: 10

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 316 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°10 :

```

40  1  AGAAAGCAGT CATATTGGCC ATCCACAGGT CACAATGGTT CTCTCCTTGA
    51  CCTGGCATCG GGATTCGAAG TATGGTGCAG TTCACGTAGT TGGAATACAA
    101  CACGAAATGT GTTCGTTGGT ACGCCAATAG GGGTTCTCGC AAAGAACATA
45  151  TCATTTGGAG GAAGGCGTAG TCCGTCGAGA TATCCCAAAA CTAGGGTTTC
    201  ATTGCGTGCG AACCAACTGC CCCCACTTCT GTATGTGTAC TGTAAGGAGT
    251  RGTGAACGG YGTCCTCTTT CCCATAACCT TGAAGTTTTT AACTGCAGA
50  301  GGATTACCTC TCAAAA

```



## (11) INFORMATION FOR SEQ ID N°: 11

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 241 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°11 :

```

1  AAGGTAGCAA GGGTGGTAGG CTTTCCTCAC AAAGAGTCTG GCTTCCGTGA
15  51  TAACCATATC CATTCTCAC CGTATACCCG TCATCCAACG TCAATTGTGT
    101  TACAAGGCAG ATAATGTCAA AATGGCTCTG GTCCCTATAA TAGTCGGATA
    151  ATGTAGAAAT CGCTCCATGT GGCCAAATAG ATGTTCTCTT TTCATACTGT
20  201  TTTAACTTTA ATTGTAGGTC CGCCTCGTTC TCGAGGTATG T

```

## (12) INFORMATION FOR SEQ ID N°: 12

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 636 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°12 :

```

1  TTCCCCNAAT TGGCCTTGCG ANNCTTGCAA GTCGACNCTA GAGGCTCCGA
40  51  AGATGGACAG ATTGCGCATG AAATATTTGA AATCGAGCAG AATGGTGATT
    101  TTAGGAGCGA TTATATTGTG CCACCCAGTT TGAAAGTGCA AGAACGCACA
    151  GTGGTTTACC GTAACAAGTA CACCAGAGTT CCTGTAAATT TTACCGTCGA
45  201  AGTTGCCATG CTGATTGATA AGTATTTATA CWAGGAGTTC AAGAACGAGA
    251  GCCACATCGT ACCGTACCTG GCTATGATAC TGACTTTGAT AAATCTGAGG
    301  TATGCCGACA CACATGACCC GTACATCCAG TTTCTTCTCA CACAAGTGTT
50  351  CGTGGGGA AW WCTGGCGATC ATATGGGCCA CATGCCCTTC CGACGAGCGT
    401  TCTTGTTT CAG GCGCCGGCAT TATGCGCAGT TTAGGCCCAA TMACACCTTC
55  451  CACTTGTAAT TCTCCGTTGT TGGATAGTGT AAGTGAGGCC ATTGCATCAG

```

501 CATCGTGGAA GARGCCTTCC TCCAAGTAGG AACCGCCCAT TTAGGTTTGC  
 551 TTTCCCAATC CGCCAATTTA ANTTTTAAAA AAAATTCCCC CCCCAAAAAT  
 5 601 TAATTTTTTTT TAAAGGTGGA TTGTGATTTC TCCGTT

(13) INFORMATION FOR SEQ ID N°: 13

(i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 432 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA

(iii) SEQUENCE DESCRIPTION : SEQ ID N°13 :

1 GATCCCAAAA GTGCCCCTGG ARCGACGGTT ACATCATGAG CTACGTCATA  
 51 AACTTCAAAA ACCACTTCAA ATTTTCTCCC TGCTGTGTAG AATCAATTCG  
 25 101 ATTCGTCGCA CGAGAGCGGG ACTGCCTCTA CAAAGTCAAT GCCAAGGATG  
 151 CTGTAAAAAG CCTAATATCT CTGCCCCGAT TTAGGATATC GCCAACGAGT  
 201 TTCTGTCAAT TTATGCATCC GCTTTACCGC GGTGTCCATA GCGATAAGAA  
 30 251 AGCAGGTCTG TCCGATTGCG TACAGACGTG TAGAACGGCC AAAAATCGAC  
 301 GAGGAGGCTA CCATTCTATGG ATTCACGCGG CACTTGACGG GGTTCCTTGC  
 35 351 GACAAGAGAA ACCCCAAGAA GGCCTGCATA AACGGGAAAT GCACCCTCCT  
 401 TAAGAGCATG CCCACAGAA CGTACCGGGA AT

(14) INFORMATION FOR SEQ ID N°: 14

(i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 466 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA

(iii) SEQUENCE DESCRIPTION : SEQ ID N°14 :

1 AGGGCGTTCT TTGCTTYACA GGGAAARGCA TATGGGCCAC GTGACCTTCC  
 55 51 AATGACCGCT CCAAATCTGG CATAGGTTGA AYTCGCAAGT CGTGGCGCAG

101 CAGGCCTYCC ACATTCACTC CATCCTCGTC TTTTAGGATG ACTGCCGCCA  
 151 TTTGTTTTGT ATCGTGGTAC AGGTGTTTGT TATGGTCCGA GCCGTCGACA  
 5 201 TAAGTATTGA CCAACGATCG GCCGAATGAT TACGGCTCAC CAAACACATC  
 251 AAATACCCCC GTCAAGTCAA GAGCTGGAAG CACAAAGCAT AGTATGTACA  
 301 AGATACCCCTT GGAAATCTTT CCCGAAGTTC ACCTTGTTGGT GGACAGCACA  
 10 351 TTTGCCAAAG CTTTAAATT TGACGTGTAC AAAGTAACGC GTTACTTCGC  
 401 AGTGCTTACA AATGCGGCTA ATCTTAGGTA TGCCAGCTTC GTATTTCCAA  
 15 451 AAGTACAGCT CAGGAT

(15) INFORMATION FOR SEQ ID N°: 15

20

(i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 377 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- 25 (d) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA

(iii) SEQUENCE DESCRIPTION : SEQ ID N°15 :

30

1 CTCGTCCACA CATTCTCCTA AAATGCAAGC CTTTTTTTTC CCACAAGGTG  
 51 TACCGTCGAC TACTGAGT CTCCAATAAA TATGTTTTCC GGTGCAATTT  
 35 101 ACCTTGCACT CTTTGACGCC GTATGTAGGG TCAGCGTGCA TGCCTTCGTC  
 151 GTACATATAC ACCCTCTGAC AGTAGTTGCT CAGTGTTGTC ATCCTACCAG  
 201 GAAGCTTAGA CGAACGTTTT ATTGTTTTTG TCGTGATCG TTCTCTAAGG  
 40 251 CATTTGAATT CCGGACGGTT GTAGAGGTTT CTGACTTCTC GCTGGCAGCA  
 301 ATAAGAGAAC TGATACTGGC GCTCGTCTTG CATCTGTAA CTCATGAGGT  
 45 351 ATCCGTCATC CCATGGGCAG TCCGCAG

## (16) INFORMATION FOR SEQ ID N°: 16

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 1670 base pairs  
 (b) TYPE : nucleic acid  
 (c) STRANDEDNESS : single  
 (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) FEATURE :

- (a) NAME/KEY : CDS  
 (b) LOCATION : 54 .. 1520

## (iv) SEQUENCE DESCRIPTION : SEQ ID N°16 :

```

1   AAGGAAGAAG TTAGGCGTAG GCTTTGGGAA ACCGGTCATC CTCGAAACCA GAG
54  ATG TCG GGA CTC AGC CTG AAA TTG TGG ATT GTA GCG TTC TTT TCT
20  Met Ser Gly Leu Ser Leu Lys Leu Trp Ile Val Ala Phe Phe Ser
99  TTC TGC TTG GCC GAG AAA GAG CAT GGG ATC GTG TAC CCC AGG ATG CTT
    Phe Cys Leu Ala Glu Lys Glu His Gly Ile Val Tyr Pro Arg Met Leu
25  147 GAA AGC AGA GCA GCA ACT GGA GAG AGA ATG CTT AAA ATC AAC GAT GAC
    Glu Ser Arg Ala Ala Thr Gly Glu Arg Met Leu Lys Ile Asn Asp Asp
195  CTG ACG TTG ACG CTG CAG AAG AGT AAG GTC TTC GCT GAC GAC TTT CTC
    Leu Thr Leu Thr Leu Gln Lys Ser Lys Val Phe Ala Asp Asp Phe Leu
30  243 TTC AGC ACG ACC GAC GGA ATT GAA CCT ATT GAT TAC TAC ATC AAA GCC
    Phe Ser Thr Thr Asp Gly Ile Glu Pro Ile Asp Tyr Tyr Ile Lys Ala
291  GAA GAC GCT GAA CGT GAC ATC TAC CAC GAC GCA ACT CAC ATG GCA TCA
35  Glu Asp Ala Glu Arg Asp Ile Tyr His Asp Ala Thr His Met Ala Ser
339  GTA AGG GTA ACG GAC GAT GAT GGC GTG GAA GTG GAA GGA ATT CTT GGA
    Val Arg Val Thr Asp Asp Asp Gly Val Glu Val Glu Gly Ile Leu Gly
40  387 GAG AGG CTT CGT GTT AAA CCT TTG CCG GCA ATG GCC CGC AGC AGC GAT
    Glu Arg Leu Arg Val Lys Pro Leu Pro Ala Met Ala Arg Ser Ser Asp
435  GGC CTC AGA CCG CAT ATG TTG TAC GAA GTC GAC GCA CAC GAA AAC GGC
    Gly Leu Arg Pro His Met Leu Tyr Glu Val Asp Ala His Glu Asn Gly
45  483 CGG CCA CAT GAT TAT GGT TCA CCG AAC ACA ACA AAT ACC CCC GTA GAG
    Arg Pro His Asp Tyr Gly Ser Pro Asn Thr Thr Asn Thr Pro Val Glu
531  AGA AGA GCT GGA GGC ACA GAA CCC CAG ATG TAC AAG ATA CCA GCG GAA
50  Arg Arg Ala Gly Gly Thr Glu Pro Gln Met Tyr Lys Ile Pro Ala Glu
579  ATC TAT CCC GAA GTT TAC CTT GTG GCG GAT AGT GCC TTT GCC AAA GAA
    Ile Tyr Pro Glu Val Tyr Leu Val Ala Asp Ser Ala Phe Ala Lys Glu
55  627 TTT AAC TTT GAT GTG AAC GCC GTT ACG CGT TAC TTC GCA GTG CTT ACA
    Phe Asn Phe Asp Val Asn Ala Val Thr Arg Tyr Phe Ala Val Leu Thr

```

675 AAT GCG GCT AAT CTT AGG TAT GAA AGC TTC AAA TCT CCA AAG GTA CAG  
 Asn Ala Ala Asn Leu Arg Tyr Glu Ser Phe Lys Ser Pro Lys Val Gln  
 5 723 CTC AGG ATC GTT GGC ATA ACG ATG AAC AAA AAC CCA GCA GAC GAG CCA  
 Leu Arg Ile Val Gly Ile Thr Met Asn Lys Asn Pro Ala Asp Glu Pro  
 771 TAC ATT CAC AAT ATA CGG GGA TAT GAG CAG TAC CGG AAT ATT TTG TTT  
 Tyr Ile His Asn Ile Arg Gly Tyr Glu Gln Tyr Arg Asn Ile Leu Phe  
 10 819 AAG GAA ACA CTG GAG GAT TTC AAC ACT CAG ATG AAG TCA AAA CAT TTT  
 Lys Glu Thr Leu Glu Asp Phe Asn Thr Gln Met Lys Ser Lys His Phe  
 867 TAT CGT ACT GCC GAT ATC GTG TTT CTC GTG ACA GCA AAA AAT ATG TCC  
 15 Tyr Arg Thr Ala Asp Ile Val Phe Leu Val Thr Ala Lys Asn Met Ser  
 915 GAA TGG GTT GGT AGC ACA CTA CAA TCA TGG ACT GGC GGG TAC GCT TAC  
 Glu Trp Val Gly Ser Thr Leu Gln Ser Trp Thr Gly Gly Tyr Ala Tyr  
 20 963 GTA GGA ACA GCG TGT TCC GAA TGG AAA GTA GGA ATG TGT GAA GAC CGA  
 Val Gly Thr Ala Cys Ser Glu Trp Lys Val Gly Met Cys Glu Asp Arg  
 1011 CCG ACA AGC TAT TAC GGA GCT TAC GTT TTC GCC CAT GAG CTG GCG CAT  
 25 Pro Thr Ser Tyr Tyr Gly Ala Tyr Val Phe Ala His Glu Leu Ala His  
 1059 AAT TTG GGT TGT CAA CAC GAT GGA GAT GGT GCC AAT AGC TGG GTG AAA  
 Asn Leu Gly Cys Gln His Asp Gly Asp Gly Ala Asn Ser Trp Val Lys  
 1107 GGG CAC ATC GGA TCT GCG GAC TGC CCA TGG GAT GAC GGA TAC CTT ATG  
 30 Gly His Ile Gly Ser Ala Asp Cys Pro Trp Asp Asp Gly Tyr Leu Met  
 1155 AGC TAC AAG ATG GAA GAC GAG CGC CAG TAT AAG TTT TCT CCC TAC TGC  
 Ser Tyr Lys Met Glu Asp Glu Arg Gln Tyr Lys Phe Ser Pro Tyr Cys  
 35 1203 CAG AGA GAA GTC AGG AAC CTC TAC AGG CGT CCG GAA TTC AAA TGC CTC  
 Gln Arg Glu Val Arg Asn Leu Tyr Arg Arg Pro Glu Phe Lys Cys Leu  
 1251 ACT GAA CGA AAA GCG AAA AAA ACA ATC CGC TCG TCT AAG CTA CCT GGT  
 40 Thr Glu Arg Lys Ala Lys Lys Thr Ile Arg Ser Ser Lys Leu Pro Gly  
 1299 GTG ATG ACA TCA TCG AGC AAC TAT TGC CGG AGG GTG TAC ATG TAC GAA  
 Val Met Thr Ser Ser Ser Asn Tyr Cys Arg Arg Val Tyr Met Tyr Glu  
 1347 AAA GGC ATG CAC GCC GAC GAG GCA TAT GGC GTC AAG GAC TGC AGG GTA  
 45 Lys Gly Met His Ala Asp Glu Ala Tyr Gly Val Lys Asp Cys Arg Val  
 1395 AAA TGC ACC ACC ACA TCA AGA ATG TAT TGG CTA CTC GGT GTA GTC GAC  
 Lys Cys Thr Thr Thr Ser Arg Met Tyr Trp Leu Leu Gly Val Val Asp  
 50 1443 GGT ACA CCT TGC GGA AAT GGA AAG GCT TGC ATT CTT GGG AAA TGC AGG  
 Gly Thr Pro Cys Gly Asn Gly Lys Ala Cys Ile Leu Gly Lys Cys Arg  
 1491 AAC AAA ATC AAA ATA AGC AAG AAG GAC TGA GAGGTTGATA ATATCAAATT  
 Asn Lys Ile Lys Ile Ser Lys Lys Asp End  
 55 1541 AATCATGATA TTTCAACCAC ATGACTTCGT GCTCAACTGG TAGCCCCAAA TAAATTTTAA

1601 AAAAATCCC AATATGCGTG GTAGAAAAG CAGCAAACAA TAAACTTCT AAAAATGTCT  
 1661 TGCAAAAATG

5

## (17) INFORMATION FOR SEQ ID N°: 17

## (i) SEQUENCE CHARACTERISTICS :

- 10 (a) LENGTH : 158 base pairs  
 (b) TYPE : nucleic acid  
 (c) STRANDEDNESS : single  
 (d) TOPOLOGY : linear

## 15 (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°17 :

20 1 CACCAGTGAT GCTTATTGTT GCACTGCACT TGTGATAAT ATCCGGTCGT  
 51 CGAATTGCAC TTCGGA ACTT CCACTCCAAC TTGGCGAGCC GTGGATTTTG  
 101 ACTTCTCGTG ATGCTCCACC AGACAGTTGC AGGACTTCAG CTGCCTAGAT  
 25 151 GGAGCCTT

## 30 (18) INFORMATION FOR SEQ ID N°: 18

## (i) SEQUENCE CHARACTERISTICS :

- 35 (a) LENGTH : 146 base pairs  
 (b) TYPE : nucleic acid  
 (c) STRANDEDNESS : single  
 (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°18 :

40 1 CTGTTGTTGA ACTGAAATAA ATAACAAAAA AATCATAAAG NTGGAGGAAA  
 51 GATGATCGAN TCCCCGCCCC TTGACAATCG TCCGATAAAA ACCAACTATA  
 45 101 TTCNGTCCTT TTTACAAACA ATTCCAANTG TCTGACCGAA CCGCGA

## (19) INFORMATION FOR SEQ ID N°: 19

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 140 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°19 :

```
1 CTNGGACGAN GTCCTATGAC TTGCGCTTAN GTTTCTTAGT CTTCTTCGGT
51 TTCTTCTTTT TTTGCTTCGG TTTTTCGGTG GGCGCAGGTG TATAGTCATC
101 AGTGTCGGTG GGCCCATCCG AATGAGTTGT CAAATGACAT
```

## (20) INFORMATION FOR SEQ ID N°: 20

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 143 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°20 :

```
1 TGCCGAAAAA TAACGATGAT TTGACGTTGA CTCTGCAGAA GAGTAAGGTT
51 TTCACCGACA GTTTTCTGTT TAGCACGACG AAGGATAACG AGCCTATCGA
101 TTACTACGTG AGAGCCGAAG ATGCCGAACG AGACATATAT CAC
```

## (21) INFORMATION FOR SEQ ID N°: 21

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 140 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°21 :

```
1 TGTTGCTACA GACTCGACGT TTCGAGCTTG CTCGCCATTT MAAGACAACG
51 CACTCACAGA ATATTTAAGT GCGTTCGTGA WAGCTGTGGG CTTACGATTG
```

101 CAGGCGCTTC ANTCACCAGC TGTGATATTA MAGTTCCTAG

5 (22) INFORMATION FOR SEQ ID N°: 22

(i) SEQUENCE CHARACTERISTICS :

- 10 (a) LENGTH : 144 base pairs  
(b) TYPE : nucleic acid  
(c) STRANDEDNESS : single  
(d) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA

15 (iii) SEQUENCE DESCRIPTION : SEQ ID N°22 :

1 TCACGATAGT TGAAACGTTG AAACCTGAAA TACTCCCACA GTCGTTGGAT  
51 GCTTCAGAAC TGCTAAGAAC TTCACACTTT GCAAGAAGTW CCAAAATGAA  
20 101 AGCCGCGATG ACCGATGATT TAGCTTCCAT CTTCTATCAC TTGA

25 (23) INFORMATION FOR SEQ ID N°: 23

(i) SEQUENCE CHARACTERISTICS :

- 30 (a) LENGTH : 95 base pairs  
(b) TYPE : nucleic acid  
(c) STRANDEDNESS : single  
(d) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA

35 (iii) SEQUENCE DESCRIPTION : SEQ ID N°23 :

1 GACCACCCCG TCCGAACCTG CTAAAKCAAG CAATGGAGTG AGGTGTTCTA  
51 TGCGGGTTGA TTACACCAAT GGCGCTGCGT GGTGCGTGGT GATTT  
40



## (24) INFORMATION FOR SEQ ID N°: 24

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 1414 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) FEATURE :

- (a) NAME/KEY : CDS
- (b) LOCATION : 143 .. 1276

## (iv) SEQUENCE DESCRIPTION : SEQ ID N°24 :

```

1   GTAGGGCCGT GCAAGCGAAG GCAGCGAAGG CTGCGAGTGT ACGTGCAGTT CGGAAGTGCA
61  ATATCCTGTT ATTAAGCTCT AATTAGCACA CTGTGAGTCG ATCAGAGGCC TCTCTTAACG
121 CCACATTGAA AAAGGATCCA AG ATG GAG GCA AGT CTG AGC AaC CAC ATC CTT
      Met Glu Ala Ser Leu Ser Asn His Ile Leu
173 AAC TTC TCC GTC GAC CTA TAC AAG CAG CTG AAA CCC TCC GGC AAA GAC
      Asn Phe Ser Val Asp Leu Tyr Lys Gln Leu Lys Pro Ser Gly Lys Asp
221 ACG GCA GGA AAC GTC TTC TGC TCA CCA TTC AGT ATT GCA GCT GCT CTG
      Thr Ala Gly Asn Val Phe Cys Ser Pro Phe Ser Ile Ala Ala Ala Leu
269 TCC ATG GCC CTC GCA GGA GCT AGA GGC AAC ACT GCC AAG CAA ATC GCT
      Ser Met Ala Leu Ala Gly Ala Arg Gly Asn Thr Ala Lys Gln Ile Ala
317 GCC ATC CTG CAC TCA AAC GAC GAC AAG ATC CAC GAC CAC TTC TCC AAC
      Ala Ile Leu His Ser Asn Asp Asp Lys Ile His Asp His Phe Ser Asn
365 TTC CTT TGC AAG CTT CCC AGT TAC GCC CCA GAT GTG GCC CTG CAC ATC
      Phe Leu Cys Lys Leu Pro Ser Tyr Ala Pro Asp Val Ala Leu His Ile
413 GCC AAT CGC ATG TAC TCT GAG CAG ACC TTC CAT CCG AAA GCG GAG TAC
      Ala Asn Arg Met Tyr Ser Glu Gln Thr Phe His Pro Lys Ala Glu Tyr
461 ACA ACC CTG TTG CAA AAG TCC TAC GAC AGC ACC ATC AAG GCT GTT GAC
      Thr Thr Leu Leu Gln Lys Ser Tyr Asp Ser Thr Ile Lys Ala Val Asp
509 TTT GCA GGA AAT GCC GAC AGG GTC CGT CTG GAG GTC AAT GCC TGG GTT
      Phe Ala Gly Asn Ala Asp Arg Val Arg Leu Glu Val Asn Ala Trp Val
557 GAG GAA GTC ACC AGG TCA AAG ATC AGG GAC CTG CTC GCA CCT GGA ACT
      Glu Glu Val Thr Arg Ser Lys Ile Arg Asp Leu Leu Ala Pro Gly Thr
605 GTT GAT TCA TCG ACA TCA CTT ATA TTA GTG AAT GCC ATT TAC TTC AAA
      Val Asp Ser Ser Thr Ser Leu Ile Leu Val Asn Ala Ile Tyr Phe Lys
653 GGT CTG TGG GAT TCT CAG TTC AAG CCT AGT GCT ACG AAG CCG GGA GAT
      Gly Leu Trp Asp Ser Gln Phe Lys Pro Ser Ala Thr Lys Pro Gly Asp

```

701 TTT CAC TTG ACA CCA CAG ACC TCA AAG AAA GTG GAC ATG ATG CAC CAG  
 Phe His Leu Thr Pro Gln Thr Ser Lys Lys Val Asp Met Met His Gln  
 5 749 GAA GGG GAC TTC AAG ATG GGT CAC TGC AGC GAC CTC AAG GTC ACT GCG  
 Glu Gly Asp Phe Lys Met Gly His Cys Ser Asp Leu Lys Val Thr Ala  
 797 CTT GAG ATA CCC TAC AAA GGC AAC AAG ACG TCG ATG GTC ATT CTC CTG  
 Leu Glu Ile Pro Tyr Lys Gly Asn Lys Thr Ser Met Val Ile Leu Leu  
 10 845 CCC GAA GAT GTA GAG GGA CTC TCA GTC CTG GAG GAA CAC TTG ACC GCT  
 Pro Glu Asp Val Glu Gly Leu Ser Val Leu Glu Glu His Leu Thr Ala  
 893 CCG AAA CTG TCG GCT CTG CTC GGC GGC ATG TAT GCG ACG TCC GAT GTC  
 Pro Lys Leu Ser Ala Leu Leu Gly Gly Met Tyr Ala Thr Ser Asp Val  
 15 941 AAC TTG CGC TTG CCG AAG TTC AAA CTA GAG CAG TCC ATA GGT TTG AAG  
 Asn Leu Arg Leu Pro Lys Phe Lys Leu Glu Gln Ser Ile Gly Leu Lys  
 989 GAT GTA CTG ATG GCG ATG GGA GTC AAG GAT TTC TTC ACG TCC CTT GCA  
 20 Asp Val Leu Met Ala Met Gly Val Lys Asp Phe Phe Thr Ser Leu Ala  
 1037 GAT CTT TCT GGC ATC AGC GCT GCG GGG AAT CTG TGC GCT TCG GAT GTC  
 Asp Leu Ser Gly Ile Ser Ala Ala Gly Asn Leu Cys Ala Ser Asp Val  
 25 1085 ATC CAC AAG GCT TTT GTG GAA GTT AAT GAG GAG GGC ACA GAG GCT GCA  
 Ile His Lys Ala Phe Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala  
 1133 GCT GCC ACT GCC ATA CCC ATT ATG TTG ATG TGT GCG AGA TTT CCA CAG  
 Ala Ala Thr Ala Ile Pro Ile Met Leu Met Cys Ala Arg Phe Pro Gln  
 30 1181 GTG GTG AAC TTT TTC GTT GAC CGC CCA TTC ATG TTC TTG ATC CAC AGC  
 Val Val Asn Phe Phe Val Asp Arg Pro Phe Met Phe Leu Ile His Ser  
 1229 CAT GAT CCA GAT GTT GTT CTC TTC ATG GGA TCC ATC CGT GAG CTC TAA  
 35 His Asp Pro Asp Val Val Leu Phe Met Gly Ser Ile Arg Glu Leu End  
 1277 AAAGCATATT CTTAACGGCG GCCAATCAGT CTGTGGAGTT ATCTCTTAGT CACTAATGTG  
 1337 TAACAATTCT GCAATATTCA GCTTGTGTAT TTCAGTAACT TGCTAGATCT TTGTGTTGTT  
 40 1397 GATGTTAGGC TTCTTGCG

## (25) INFORMATION FOR SEQ ID N°: 25

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 200 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°25 :

```

1  ACCGTAACCA AAATTGTTTC TTTCCAGAAG AATGGTTCAA ACTTTTCAAA
51  CAGATTTTCGG AAACCTCTTCT TGCACCTTTTA AAATCCAATC TACAATCTTT
101 CCTCGCACTT CTGAATTGCA TTCCAGTTTA CCTTCCAAGC AAACCTCTTT
151 TGGCAACTCC AGCCGTACTC CATTTTCGGCA TACCACAGTG CATGCACTTG

```

## (26) INFORMATION FOR SEQ ID N°: 26

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 241 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°26 :

```

1  CGTATTCTTT GAAGATTTGT ATACGAAACA TAAATTCGTC ATGCATACTT
51  TTGATGGTTA CACGACATGC GAAGCTGCCG ACAAAGAAGA CTGGGAAGAT
101 AAGAAGCACC TAGTTACGGT AGTGCGTGGA CCGGATAAAC GAAAGTACAC
151 GTTTCTACGC AACATTCTCA CCTTACAACG GAGAGTGAGA GTTAGCAAAA
201 CAATGATTGA GTCGTACGG AACATGTCCT GTAGGACATT T

```

## (27) INFORMATION FOR SEQ ID N°: 27

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 313 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) SEQUENCE DESCRIPTION : SEQ ID N°27 :

```

1   AAGCANCCGG ACTACCTGCT TGAAAACGTT GTACGGGCAA ACTTGGACGG
15  51   AAAACTCCCA GATGCTACTC CAGTTCCTCC CGGAAGCTAC ACGTACGCTG
    101  AGAATGATAA CTTACCTGCT TATTCAGAA GTACACCGTT TCCGGATGGG
    151  GTGAATGTTG TATAACGGCT GCTGGGTGCG GAAGACTATG ATGGATTACG
20  201  CAAAAAAGTT CTAAACGAGT TGTTTCCCAT CCCGAAAGT CTGCTGTATG
    251  CTGACATGAT GCGACTTGTG GCTAAGAAAG ACAGAGTTGA TCACACTAGT
25  301  GGATGACCTG GGA

```

## (28) INFORMATION FOR SEQ ID N°: 28

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 2417 base pairs
- (b) TYPE : nucleic acid
- (c) STRANDEDNESS : single
- (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) FEATURE :

- (a) NAME/KEY : CDS
- (b) LOCATION : 218 .. 1495

## (iv) SEQUENCE DESCRIPTION : SEQ ID N°28 :

```

45  1   GTCGTAGTCG TAGTCGTAGT CAGTTGCGCA TGCGCGGGGC TTTCCTGTCT TTCTTGCCTT
    61   TCTGCAGTCG TTCACCAACA TGTGGATACA GCTCCGGAGA TTTGTAAACA AATACTGCAC
    121  TTTTAAGCAA GACTTGATAT TTAGATCGAT ATCCTCCTGT TGTCCGTCTT GATTAATCGG
50  181  CTCTTTAGGG TTTTLAGAAT AGGCTTTTCG GTACGAG ATG CCC AAA GGA AAG AGG
                                   Met Pro Lys Gly Lys Arg
    236  GGA CCC AAA GCA GGT GGC GCC GCG CGC GGT GGC CGG TGC GAG GCC AGC
55  Gly Pro Lys Ala Gly Gly Ala Ala Arg Gly Gly Arg Cys Glu Ala Ser

```

	284	CTG GCT CCG TCg TCC AGC GAC GAG GAG TCC AAC GCA GAC ACG GCG AGC
		Leu Ala Pro Ser Ser Ser Asp Glu Glu Ser Asn Ala Asp Thr Ala Ser
5	332	GTG CTG AGC TGC GCC TCG GAG TCT CGC TGT GGC AGT GAC GGC ACC GTT
		Val Leu Ser Cys Ala Ser Glu Ser Arg Cys Gly Ser Asp Gly Thr Val
	380	GGA GAC CCA GAA GCG GAG GAG GCT GTG CTG CAT GAC GAC TTT GAA GAC
		Gly Asp Pro Glu Ala Glu Glu Ala Val Leu His Asp Asp Phe Glu Asp
10	428	AAA CTC AAG GAG GCC ATC GAC GGA GCT TCG CAG AAG AGT GCC AAA GGA
		Lys Leu Lys Glu Ala Ile Asp Gly Ala Ser Gln Lys Ser Ala Lys Gly
	476	CGG CTG TCG TGC CTG GAG GCG ATT CGC AAG GCC TTT TcC ACC AAA TAC
		Arg Leu Ser Cys Leu Glu Ala Ile Arg Lys Ala Phe Ser Thr Lys Tyr
15	524	CTG TAC GAC TTC CTC ATG GAC AGA CCG AGC ACG GTG TGC GAC CTG GTG
		Leu Tyr Asp Phe Leu Met Asp Arg Pro Ser Thr Val Cys Asp Leu Val
	572	GAG CGT GGG GTG CGC AAG GGC CGA GGG GAG GAG GCG GCC CTG TGC GCC
20		Glu Arg Gly Val Arg Lys Gly Arg Gly Glu Glu Ala Ala Leu Cys Ala
	620	ACT CTC GGG GCC CTG GCC TGC GTC CAG CTC GGG GTC GGG GCC GAG GCG
		Thr Leu Gly Ala Leu Ala Cys Val Gln Leu Gly Val Gly Ala Glu Ala
25	668	GAC GCC CTG TTC GAC GCC CTG CGC CAG CCG CTC TGC ACT TTG CTG CTT
		Asp Ala Leu Phe Asp Ala Leu Arg Gln Pro Leu Cys Thr Leu Leu Leu
	716	GAC GGG GCC CAG GGG CCC TCC CCC AGG GCC AGG TGT GCC ACT GCC CTC
30		Asp Gly Ala Gln Gly Pro Ser Pro Arg Ala Arg Cys Ala Thr Ala Leu
	764	GGC CTC TGC TGc TTC GTG GTG GAC TCG GAC AAC CAG CTG GTG CTG CAG
		Gly Leu Cys Cys Phe Val Val Asp Ser Asp Asn Gln Leu Val Leu Gln
35	812	CCG TGC ATG GAG GTG CTC TGG CAG GTG GTG GGT GCC AAG GCG GGC CCC
		Pro Cys Met Glu Val Leu Trp Gln Val Val Gly Ala Lys Ala Gly Pro
	860	GGC TCT CCG GTG CTC CAG GCA GCG GCC CTG CTC GCC TGG GGC CTC CTG
		Gly Ser Pro Val Leu Gln Ala Ala Ala Leu Leu Ala Trp Gly Leu Leu
40	908	CTC AGC GTG GCT CCC GTC GAC CGc CTG CTG GCG CTc ACG CGC ACG CAC
		Leu Ser Val Ala Pro Val Asp Arg Leu Leu Ala Leu Thr Arg Thr His
	956	CTG CCC CGG CTG CAG GAG CTG CTG GAG AGC CCC GAC CTG GAC CTG CGC
45		Leu Pro Arg Leu Gln Glu Leu Leu Glu Ser Pro Asp Leu Asp Leu Arg
	1004	ATT GCG GCC GGG GAG GTG ATC GCC GTC ATG TAC GAG GGG GCC AGG GAC
		Ile Ala Ala Gly Glu Val Ile Ala Val Met Tyr Glu Gly Ala Arg Asp
50	1052	TAC GAC GAG GAC TTT GAG GAG CCC TCG GAG TCC CTG TGT GCC CAG CTG
		Tyr Asp Glu Asp Phe Glu Glu Pro Ser Glu Ser Leu Cys Ala Gln Leu
	1100	CGC CAG CTG GCC ACG GAC AGC CAG AAG TTT CGG GCC AAG AAG GAG CGG
		Arg Gln Leu Ala Thr Asp Ser Gln Lys Phe Arg Ala Lys Lys Glu Arg
55	1148	CGC CAG CAG CGC TCC ACC TTC AGG GAC GTC TAC CGG GCC GTC AGG GAG
		Arg Gln Gln Arg Ser Thr Phe Arg Asp Val Tyr Arg Ala Val Arg Glu

1196 GGG GCC TCT CCC GAC GTG AGC GTC AAG TTT GGC CGG GAA GTC CTG GAA  
 Gly Ala Ser Pro Asp Val Ser Val Lys Phe Gly Arg Glu Val Leu Glu  
 5 1244 CTG GAC ACC TGG AGT CGC AAG CTG CAG TAC GAC GCT TTC TGC CAG CTG  
 Leu Asp Thr Trp Ser Arg Lys Leu Gln Tyr Asp Ala Phe Cys Gln Leu  
 1292 CTG GGC TCC GGC ATG AAC CTG CAC CTG GCC GTG AAC GAG CTG CTG AGG  
 Leu Gly Ser Gly Met Asn Leu His Leu Ala Val Asn Glu Leu Leu Arg  
 10 1340 GAC ATC TTT GAA CTG GGG CAG GTG CTG GCA ACC GAG GAC CAC ATT ATC  
 Asp Ile Phe Glu Leu Gly Gln Val Leu Ala Thr Glu Asp His Ile Ile  
 1388 TCC AAG ATC ACC AAG TTC GAA AGG CAC ATG GTG AAC ATG GCC AGC TGC  
 Ser Lys Ile Thr Lys Phe Glu Arg His Met Val Asn Met Ala Ser Cys  
 15 1436 CGG GCC CGC ACC AAG ACA CGC AAC CGG CTG AGG GAC AAG CGC GCC GAC  
 Arg Ala Arg Thr Lys Thr Arg Asn Arg Leu Arg Asp Lys Arg Ala Asp  
 1484 GTG GTC GCC TGA ACCTGCGGAG GGATGCTTAG CTATGCACTC GCCGGCCTAC  
 20 Val Val Ala End  
 1536 CCTGGCGGGA CTCGATGCCA CTCACGAGTC GGCGCTCGCA AATTCGCCGC CCATCGTTAC  
 1596 GCAATGGGAG ACAAAGCTGC TTTTGGCATT ACCGTTTGAG GTCGGCTCCA ACCCATAGAT  
 25 1656 GAATTTCTTT TTTGTGGCCG TTTCTGGGTT ACATGTTTTG GGGGAAGGGA GTGGAAGTGT  
 1716 CCGGTTCTTT GGCACACGTC AGGTTGCTCT TGATGCGCGA CGTGCTTGTA TTTGGGtACT  
 30 1776 GCCGACACCA AGCGTTTCGG CGATTCTTGG AAAAGAGTGC CTCTCGCTCG ACGTTTGGTT  
 1836 GTTTTCTGCG TGGTCCGTCG TCGACCTTCG TTCGTCCAAA GACGCCGTCC GGTTTCatAC  
 1896 TCCCCCCCCG ACACATATCG AGGCCAATTA AATTGCTAAG GGTGCCGTTG TCGTGCACTCT  
 35 1956 GGCAGGCTCA GAAGTGGCTT ATTTGTCTTT TAATTTTGCC GATGCACGCA AAAATTGTCA  
 2016 TTTCTTGAAA GTTTCTCTTT TATTGCGTAC ACAATTCAAC TTTTATGTAA TTTCTGATGG  
 40 2076 TCTGTTTTAC GTGTGCGTGT GTAAAACGTA ACTTTGGAAG AATTTTATG CACACTGAAC  
 2136 AAACGCTCGG TCCTGGGGTT GAAAGTGCTC GGTGTGTGCA TGAGCTAAAG TGCAACTGCT  
 2196 TTGTTCCGAA GGTTTTCTAG TCGCCGAAAT GTACCATTGT GGACCTTGTT GCGAGAGACC  
 45 2256 TTGGTCTTCT GGGGGAGCTG CTGTAGCGTG GCAAGCCACT ATTTTGGGAG CGACATTGCA  
 2316 GAGAAAATCG GCTTTTAGAA AGGCACCTGC GCGGCGAGTG GACGTTTTTTT CGTATATACT  
 50 2376 GCGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA

## (29) INFORMATION FOR SEQ ID N°: 29

## (i) SEQUENCE CHARACTERISTICS :

- (a) LENGTH : 933 base pairs  
 (b) TYPE : nucleic acid  
 (c) STRANDEDNESS : single  
 (d) TOPOLOGY : linear

## (ii) MOLECULE TYPE : cDNA

## (iii) FEATURE :

- (a) NAME/KEY : CDS  
 (b) LOCATION : 32 .. 853

## (iv) SEQUENCE DESCRIPTION : SEQ ID N°29 :

```

1      GATTGGGAAC CTCCTATTCC TCACTTGAAA C ATG GCT GGA CTC CGC TCC
      Met Ala Gly Leu Arg Ser

20  50   TGC ATC CTC CTG GCT CTT GCC ACT AGT GCC TTC GCC GGC TAC CTT CAC
      Cys Ile Leu Leu Ala Leu Ala Thr Ser Ala Phe Ala Gly Tyr Leu His

      98   GGT GGC CTT ACC CAC GGC GCT GGG TAC GGT TAC GGT GTC GGC TAC GGT
      Gly Gly Leu Thr His Gly Ala Gly Tyr Gly Tyr Gly Val Gly Tyr Gly

25  146   TCC GGC CTT GGC TAT GGC CTT GGC TAC GGT TCC GGC CTT GGC TAT GGA
      Ser Gly Leu Gly Tyr Gly Leu Gly Tyr Gly Ser Gly Leu Gly Tyr Gly

      194   CAT GCT GTT GGC CTT GGA CAC GGC TTT GGC TAT TCT GGT CTG ACC GGC
      His Ala Val Gly Leu Gly His Gly Phe Gly Tyr Ser Gly Leu Thr Gly

      242   TAC AGT GTG GCT GCC CCA GCT AGC TAC GCC GTT GCT GCT CCA GCC GTC
      Tyr Ser Val Ala Ala Pro Ala Ser Tyr Ala Val Ala Ala Pro Ala Val

35  290   AGC CGC ACC GTT TCC ACT TAC CAC GCT GCT CCA GCT GTG GCC ACC TAC
      Ser Arg Thr Val Ser Thr Tyr His Ala Ala Pro Ala Val Ala Thr Tyr

      338   GCC GCT GCT CCT GTC GCC ACC TAT GCT GTT GCT CCA GCT GTC ACT AGG
      Ala Ala Ala Pro Val Ala Thr Tyr Ala Val Ala Pro Ala Val Thr Arg

40  386   GTT TCC CCC GTT CGC GCC GCC CCA GCT GTG GCC ACG TAC GCC GCC GCT
      Val Ser Pro Val Arg Ala Ala Pro Ala Val Ala Thr Tyr Ala Ala Ala

      434   CCA GTC GCC ACC TAC GCC GCT GCT CCA GCT GTG ACC AGG GTG TCC ACC
      Pro Val Ala Thr Tyr Ala Ala Ala Pro Ala Val Thr Arg Val Ser Thr

45  482   ATT CAC GCT GCC CCG GCT GTG GCC AAT TAC GCC GTC GCT CCA GTC GCC
      Ile His Ala Ala Pro Ala Val Ala Asn Tyr Ala Val Ala Pro Val Ala

      530   ACC TAT GCC GCT GCT CCA GCT GTG ACC AGG GTG TCC ACC ATC CAC GCC
      Thr Tyr Ala Ala Ala Pro Ala Val Thr Arg Val Ser Thr Ile His Ala

      578   GCT CCA GCC GTG GCT AGC TAC CAG ACC TAC CAC GCT CCA GCT GTC GCC
      Ala Pro Ala Val Ala Ser Tyr Gln Thr Tyr His Ala Pro Ala Val Ala

55  626   ACT GTG GCT CAT GCT CCA GCT GTG GCC AGC TAC CAG ACC TAC CAC GCT

```

Thr Val Ala His Ala Pro Ala Val Ala Ser Tyr Gln Thr Tyr His Ala  
 674 GCC CCA GCC GTG GCT ACC TAC GCC CAT GCC GCT CCC GTC TAC GGC TAT  
 Ala Pro Ala Val Ala Thr Tyr Ala His Ala Ala Pro Val Tyr Gly Tyr  
 5 722 GGT GTC GGT ACC CTC GGA TAT GGT GTC GGC CAC TAC GGC TAC GGA CAC  
 Gly Val Gly Thr Leu Gly Tyr Gly Val Gly His Tyr Gly Tyr Gly His  
 770 GGT CTT GGC AGC TAC GGC CTG AAC TAC GGT TAC GGC CTC GGC ACC TAC  
 10 Gly Leu Gly Ser Tyr Gly Leu Asn Tyr Gly Tyr Gly Leu Gly Thr Tyr  
 818 GGT GAC TAC ACC ACC CTT CTC CGC AAG AAG AAG TAA ATGGCA CATCTCAAGA  
 Gly Asp Tyr Thr Thr Leu Leu Arg Lys Lys Lys End  
 15 870 GAGCCCAT TG GACTGCCATC GACATTCTTC TTCAATAAAA GAGCCCGAAG ATGGCATTAT  
 930 TTTT



## Bibliography.

- 5     Ganapamo et al, 1997 : Identification of an *Ixodes ricinus* salivary gland fraction through its ability to stimulate CD4 T cells present in BALB/c mice lymph nodes draining the tick fixation site. Ganapamo-F; Rutti-B; Brossard-M. *Parasitology*; 1997 Jul; 115 ( Pt 1): 91-6
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- 15    Ganapamo et al, 1996 : Immunosuppression and cytokine production in mice infested with *Ixodes ricinus* ticks: a possible role of laminin and interleukin-10 on the in vitro responsiveness of lymphocytes to mitogens. Ganapamo-F; Rutti-B; Brossard-M. *Immunology*; 1996 Feb; 87(2): 259-63
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- 30    Frohman, 1995 : Rapid amplification of cDNA Ends. In PCR Primer. A laboratory manual (Dieffenbach, C. W. and Dveksler, G. S., eds), pp.381-409, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.

## CLAIMS

1. A method for characterising genes which are induced in the salivary glands of a tick during the tick feeding phase which  
5 comprises :

a) selectively cloning mRNAs induced during the tick feeding phase to obtain a corresponding cDNA library ;

10 b) cloning full-length cDNAs corresponding to ~~some~~ <sup>at least one</sup> incomplete cDNA sequences identified in the library obtained in step a).

2. The method of claim 1, wherein said tick is a *Ixodes ricinus* tick.  
15

3. The method of claim 2, wherein the genes induced are induced during the slow-feeding phase of the blood meal.

20 4. The method of any of claims 1-3, which comprises :

a) synthesising uninduced cDNAs starting from mRNAs expressed in the salivary gland of unfed ticks ;

25 b) synthesising induced cDNAs starting from mRNAs expressed in the salivary gland of fed ticks ;

c) sub~~s~~tracting said uninduced cDNAs from said induced cDNAs ;  
30

d) isolating and cloning specifically induced cDNAs, thus obtaining a sub~~s~~tractive library ;

e) obtaining corresponding full-length induced cDNA ;  
35

f) sequencing and comparing said full-length induced DNA molecules with known-polypeptide and polynucleotide sequences.

5                    5. The method of claim 4, wherein a full-length cDNA library is set up and screened by means of incomplete cDNAs isolated from the sub~~s~~tractive library.

10                    6. The method of claim 4, which comprises :

a) randomly sequencing a number of clones of said sub~~s~~tractive library ;

15                    b) comparing their DNA and amino acid translated sequences with DNA and protein databases ;

c) identifying distinct family sequences ;

20                    d) characterising their corresponding full-length mRNA sequence.

7. A polynucleotide <sup>or isolatable</sup> isolated/ from tick salivary glands, which encodes a tick salivary gland polypeptide, and fragments thereof, and any closely related or complementary polynucleotide.

25                    8. The polynucleotide of claim 7, whenever obtained <sup>or obtainable</sup> from *Ixodes ricinus* salivary glands.

30                    9. The polynucleotide of claim 7, which is complementary to a *Ixodes ricinus* salivary gland cDNA.

10. <sup>A</sup> ~~The~~ polynucleotide <sup>according to any one</sup> of claims ~~8 and~~ <sup>7 to</sup> 9 having a nucleotide sequence selected from the group consisting of seq. id. no. 1, seq. id. no. 2, seq. id. no. 3, seq. id. no. 4, seq. id. no. 5, seq. id. no. 6, seq. id. no. 7, seq. id. no. 8, seq. id. no. 9, seq. id. no. 10, seq. id. no. 11, seq. id. no. 12, seq. id. no. 13, seq. id. no. 14, seq. id. no.

15, seq. id. no. 16, seq. id. no. 17, seq. id. no. 18, seq. id. no. 19, seq. id. no. 20, seq. id. no. 21, seq. id. no. 22, seq. id. no. 23, seq. id. no. 24, seq. id. no. 25, seq. id. no. 26, seq. id. no. 27, seq. id. no. 28, seq. id. no. 29, or a sequence complementary thereto, or a fragment thereof.

5

11. The polynucleotide of any of claims 7-10, further including a polynucleotide having over its entire length at least 75% identity to a nucleotide sequence encoding the *Ixodes ricinus* salivary gland polypeptide encoded by a polynucleotide as defined in claim 10.

10

12. The polynucleotide of any of claims 7-10, further including a polynucleotide comprising a nucleotide sequence that is at least 75% identical with a nucleotide sequence as defined in claim 10.

15

13. The polynucleotide of any of claims 7-10 further including a nucleotide sequence which has sufficient identity to a nucleotide sequence as defined in claim 10 to hybridize under conditions useable for amplification or for use as a probe or marker.

20

14. An isolated polypeptide encoded by the polynucleotide of claims 7-13.

25

15. An immunological composition or vaccine for inducing an immunological response in a mammalian host to a tick salivary gland polypeptide which comprises at least one member of the group consisting of

a) a tick salivary gland cDNA as defined in any of claims 7-14 ;

30

b) a tick salivary gland polypeptide as defined in claim 14 ;

c) epitope-bearing fragments, analogs, outer-membrane vesicles or cells (attenuated or otherwise) of components (a) or (b) ;

35

d) possibly a carrier.

16. A therapeutics agent having anticoagulant properties containing at least one polypeptide encoded by a polynucleotide having a nucleotide sequence selected from the group consisting of seq. id. no. 7, seq. id. no. 16, seq. id. no. 24, and fragments thereof.

17. A therapeutics agent having immunomodulatory properties containing at least one polypeptide encoded by a polynucleotide having a nucleotide sequence selected from the group consisting of seq. id. no. 11, seq. id. no. 17, seq. id. no. 19, seq. id. no. 28, and seq. id. no. 29, and fragments thereof.

18. A therapeutics agent as claimed in any of claims 16 and 17 for use alone or in combination with an anti-tick vaccine, among others as defined in claim 15, to prevent the transmission of pathogens carried by the ticks.

19. A polynucleotide which is identical or sufficiently identical to a nucleotide sequence selected from the group consisting of seq. id. no. 1, seq. id. no. 2, seq. id. no. 3, seq. id. no. 4, seq. id. no. 5, seq. id. no. 6, seq. id. no. 7, seq. id. no. 8, seq. id. no. 9, seq. id. no. 10, seq. id. no. 11, seq. id. no. 12, seq. id. no. 13, seq. id. no. 14, seq. id. no. 15, seq. id. no. 16, seq. id. no. 17, seq. id. no. 18, seq. id. no. 19, seq. id. no. 20, seq. id. no. 21, seq. id. no. 22, seq. id. no. 23, seq. id. no. 24, seq. id. no. 25, seq. id. no. 26, seq. id. no. 27, seq. id. no. 28, seq. id. no. 29 or a sequence complementary thereto, or a fragment thereof, for use as a hybridisation probe for cDNA clones encoding tick, more particularly *Ixodes ricinus*, salivary gland polypeptides ; or for isolating clones of other genes similar to tick salivary gland cDNAs.

20. A diagnostic kit for a disease or susceptibility to a disease which comprises :

(a) a tick salivary gland polynucleotide, preferably the nucleotide sequence of one of the gene sequences defined in claim 10, or a fragment thereof;

(b) a nucleotide sequence complementary to that of(a);

5 (c) a tick salivary gland polypeptide, preferably the polypeptide encoded by one of the gene sequences defined in claim 10, or a fragment thereof;

(d) an antibody to a tick salivary gland polypeptide, preferably to the polypeptide encoded by one of the gene sequences  
10 defined in claim 10; or

(e) a phage displaying an antibody to a tick salivary gland polypeptide, preferably to the polypeptide encoded by one of the cDNAs sequences defined in claim 10 whereby (a), (b), (c), (d) or (e) may comprise a substantial component.

15

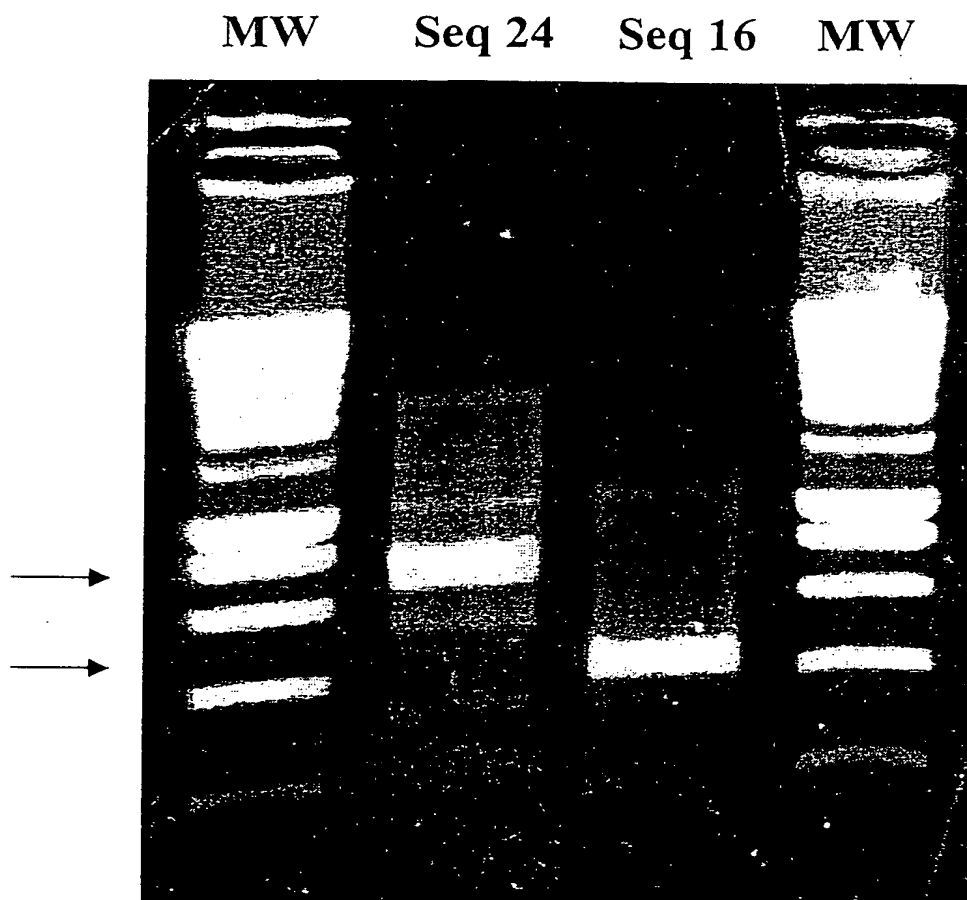


Figure 1.





	RT-PCR		PCR		E	UF
	Engorged	Unfed	Engorged	Unfed		
Seq 24					++	+
Seq 28					+	+
Seq 29					+	-
Seq 16					++	+
Seq 7					+	-
Seq 6					+	-
Seq 26					+	-
Seq 17					++	+
Seq 3					+	-
Seq 2					+	-
Seq 1					+	-
Seq 4					+	-
Seq 5					+	-
Seq 19					++	+

**FIGURE 2.**

